

# David D Pollock

## List of Publications by Year in descending order

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Version: 2024-02-01

110  
papers

11,404  
citations

61687

45  
h-index

39744

98  
g-index

128  
all docs

128  
docs citations

128  
times ranked

17084  
citing authors

#	ARTICLE	IF	CITATIONS
1	A genomic can of worms for schistosome host-specificity. <i>Trends in Parasitology</i> , 2022, 38, 496-497.	1.5	1
2	Patterns of relatedness and genetic diversity inferred from whole genome sequencing of archival blood fluke miracidia ( <i>Schistosoma japonicum</i> ). <i>PLoS Neglected Tropical Diseases</i> , 2021, 15, e0009020.	1.3	8
3	SARS-CoV-2 evolution during treatment of chronic infection. <i>Nature</i> , 2021, 592, 277-282.	13.7	802
4	Population genomic analyses of schistosome parasites highlight critical challenges facing endgame elimination efforts. <i>Scientific Reports</i> , 2021, 11, 6884.	1.6	8
5	Selection for cooperativity causes epistasis predominately between native contacts and enables epistasis-based structure reconstruction. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	5
6	Viral CpG Deficiency Provides No Evidence That Dogs Were Intermediate Hosts for SARS-CoV-2. <i>Molecular Biology and Evolution</i> , 2020, 37, 2706-2710.	3.5	18
7	Amalgamated cross-species transcriptomes reveal organ-specific propensity in gene expression evolution. <i>Nature Communications</i> , 2020, 11, 4459.	5.8	46
8	Finding and extending ancient simple sequence repeat-derived regions in the human genome. <i>Mobile DNA</i> , 2020, 11, 11.	1.3	20
9	Society for Molecular Biology and Evolution, Council and Business Meetings, 2018, Yokohama, Japan. <i>Molecular Biology and Evolution</i> , 2019, 36, 204-206.	3.5	0
10	Society for Molecular Biology and Evolution, Council and Business Meetings, 2017, Austin, TX. <i>Molecular Biology and Evolution</i> , 2018, 35, 259-261.	3.5	0
11	Biliverdin Reductase B Dynamics Are Coupled to Coenzyme Binding. <i>Journal of Molecular Biology</i> , 2018, 430, 3234-3250.	2.0	22
12	Genome of the pitcher plant <i>Cephalotus</i> reveals genetic changes associated with carnivory. <i>Nature Ecology and Evolution</i> , 2017, 1, 59.	3.4	99
13	Sequence entropy of folding and the absolute rate of amino acid substitutions. <i>Nature Ecology and Evolution</i> , 2017, 1, 1923-1930.	3.4	46
14	Mechanistic Models of Protein Evolution. , 2017, , 277-296.		3
15	Whole Genome Amplification and Reduced-Representation Genome Sequencing of <i>Schistosoma japonicum</i> Miracidia. <i>PLoS Neglected Tropical Diseases</i> , 2017, 11, e0005292.	1.3	23
16	Platform technology to generate broadly cross-reactive antibodies to $\alpha$ -helical epitopes in hemagglutinin proteins from influenza A viruses. <i>Biopolymers</i> , 2016, 106, 144-159.	1.2	10
17	The tangled bank of amino acids. <i>Protein Science</i> , 2016, 25, 1354-1362.	3.1	40
18	Parallel and Convergent Molecular Evolution. , 2016, , 206-211.		1

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19	Contrasting patterns of evolutionary diversification in the olfactory repertoires of reptile and bird genomes. <i>Genome Biology and Evolution</i> , 2016, 8, evw013.	1.1	28
20	Squamate Reptile Genomics and Evolution. , 2016, , 29-49.		0
21	Rapid changes in gene expression direct rapid shifts in intestinal form and function in the Burmese python after feeding. <i>Physiological Genomics</i> , 2015, 47, 147-157.	1.0	28
22	Nonadaptive Amino Acid Convergence Rates Decrease over Time. <i>Molecular Biology and Evolution</i> , 2015, 32, 1373-1381.	3.5	66
23	A call for benchmarking transposable element annotation methods. <i>Mobile DNA</i> , 2015, 6, 13.	1.3	83
24	Inference of Transposable Element Ancestry. <i>PLoS Genetics</i> , 2014, 10, e1004482.	1.5	13
25	Three crocodylian genomes reveal ancestral patterns of evolution among archosaurs. <i>Science</i> , 2014, 346, 1254449.	6.0	300
26	Two Antarctic penguin genomes reveal insights into their evolutionary history and molecular changes related to the Antarctic environment. <i>GigaScience</i> , 2014, 3, 27.	3.3	72
27	Strong evidence for protein epistasis, weak evidence against it. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, E1450-E1450.	3.3	31
28	The western painted turtle genome, a model for the evolution of extreme physiological adaptations in a slowly evolving lineage. <i>Genome Biology</i> , 2013, 14, R28.	13.9	276
29	The Burmese python genome reveals the molecular basis for extreme adaptation in snakes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 20645-20650.	3.3	260
30	The king cobra genome reveals dynamic gene evolution and adaptation in the snake venom system. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 20651-20656.	3.3	412
31	Chinese alligator genome illustrates molecular adaptations. <i>Cell Research</i> , 2013, 23, 1254-1255.	5.7	3
32	Amino acid coevolution induces an evolutionary Stokes shift. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, E1352-9.	3.3	183
33	SP Transcription Factor Paralogs and DNA-Binding Sites Coevolve and Adaptively Converge in Mammals and Birds. <i>Genome Biology and Evolution</i> , 2012, 4, 1102-1117.	1.1	8
34	Germline TRAV5D-4 T-Cell Receptor Sequence Targets a Primary Insulin Peptide of NOD Mice. <i>Diabetes</i> , 2012, 61, 857-865.	0.3	31
35	Transcriptome sequencing of black grouse ( <i>Tetrao tetrix</i> ) for immune gene discovery and microsatellite development. <i>Open Biology</i> , 2012, 2, 120054.	1.5	26
36	LTR Retrotransposons Contribute to Genomic Gigantism in Plethodontid Salamanders. <i>Genome Biology and Evolution</i> , 2012, 4, 168-183.	1.1	152

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37	Report from the First Snake Genomics and Integrative Biology Meeting. <i>Standards in Genomic Sciences</i> , 2012, 7, 150-152.	1.5	4
38	Phylogenetics, likelihood, evolution and complexity. <i>Bioinformatics</i> , 2012, 28, 2989-2990.	1.8	10
39	Thousands of microsatellite loci from the venomous coralsnake <i>Micrurus fulvius</i> and variability of select loci across populations and related species. <i>Molecular Ecology Resources</i> , 2012, 12, 1105-1113.	2.2	26
40	Rapid Microsatellite Identification from Illumina Paired-End Genomic Sequencing in Two Birds and a Snake. <i>PLoS ONE</i> , 2012, 7, e30953.	1.1	208
41	The interface of protein structure, protein biophysics, and molecular evolution. <i>Protein Science</i> , 2012, 21, 769-785.	3.1	188
42	Modeling Protein Evolution. <i>Biological and Medical Physics Series</i> , 2012, , 311-325.	0.3	0
43	The genome of the green anole lizard and a comparative analysis with birds and mammals. <i>Nature</i> , 2011, 477, 587-591.	13.7	575
44	Sequencing the genome of the Burmese python ( <i>Python molurus bivittatus</i> ) as a model for studying extreme adaptations in snakes. <i>Genome Biology</i> , 2011, 12, 406.	13.9	58
45	Bayesian Analysis of High-Throughput Quantitative Measurement of Protein-DNA Interactions. <i>PLoS ONE</i> , 2011, 6, e26105.	1.1	2
46	Discovery of Highly Divergent Repeat Landscapes in Snake Genomes Using High-Throughput Sequencing. <i>Genome Biology and Evolution</i> , 2011, 3, 641-653.	1.1	87
47	A proposal to sequence the genome of a garter snake ( <i>Thamnophis sirtalis</i> ). <i>Standards in Genomic Sciences</i> , 2011, 4, 257-270.	1.5	31
48	A multi-organ transcriptome resource for the Burmese Python ( <i>Python molurus bivittatus</i> ). <i>BMC Research Notes</i> , 2011, 4, 310.	0.6	18
49	Repetitive Elements May Comprise Over Two-Thirds of the Human Genome. <i>PLoS Genetics</i> , 2011, 7, e1002384.	1.5	907
50	Two-pore channels for integrative Ca <sup>2+</sup> signaling. <i>Communicative and Integrative Biology</i> , 2010, 3, 12-17.	0.6	34
51	Gene-specific RNA polymerase II phosphorylation and the CTD code. <i>Nature Structural and Molecular Biology</i> , 2010, 17, 1279-1286.	3.6	200
52	The genome of a songbird. <i>Nature</i> , 2010, 464, 757-762.	13.7	770
53	Comparison of Normalization Methods for Construction of Large, Multiplex Amplicon Pools for Next-Generation Sequencing. <i>Applied and Environmental Microbiology</i> , 2010, 76, 3863-3868.	1.4	71
54	Rapid Likelihood Analysis on Large Phylogenies Using Partial Sampling of Substitution Histories. <i>Molecular Biology and Evolution</i> , 2010, 27, 249-265.	3.5	23

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55	Adaptive molecular convergences. <i>Communicative and Integrative Biology</i> , 2010, 3, 67-69.	0.6	13
56	Rapid identification of thousands of copperhead snake ( <i>Agkistrodon contortrix</i> ) microsatellite loci from modest amounts of 454 shotgun genome sequence. <i>Molecular Ecology Resources</i> , 2010, 10, 341-347.	2.2	179
57	Dynamic Nucleotide Mutation Gradients and Control Region Usage in Squamate Reptile Mitochondrial Genomes. <i>Cytogenetic and Genome Research</i> , 2009, 127, 112-127.	0.6	22
58	Identifying DNA Strands Using a Kernel of Classified Sequences. , 2009, , .		0
59	Ancestral Sequence Reconstruction in Primate Mitochondrial DNA: Compositional Bias and Effect on Functional Inference. <i>Molecular Biology and Evolution</i> , 2009, 26, 481-481.	3.5	1
60	Evidence for an ancient adaptive episode of convergent molecular evolution. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 8986-8991.	3.3	284
61	F.44. High-throughput Parallel Pyrosequencing of T Cell Receptors from the NOD Mouse Reveals Tens of Thousands of Unique Sequences. <i>Clinical Immunology</i> , 2009, 131, S105-S106.	1.4	0
62	Intrinsic amino acid side-chain hydrophilicity/hydrophobicity coefficients determined by reversed-phase high-performance liquid chromatography of model peptides: Comparison with other hydrophilicity/hydrophobicity scales. <i>Biopolymers</i> , 2009, 92, 573-595.	1.2	114
63	Identification of repeat structure in large genomes using repeat probability clouds. <i>Analytical Biochemistry</i> , 2008, 380, 77-83.	1.1	51
64	Structural, Biochemical, and in Vivo Characterization of the First Virally Encoded Cyclophilin from the Mimivirus. <i>Journal of Molecular Biology</i> , 2008, 378, 71-86.	2.0	30
65	Adaptive Evolution and Functional Redesign of Core Metabolic Proteins in Snakes. <i>PLoS ONE</i> , 2008, 3, e2201.	1.1	113
66	An ancient adaptive episode of convergent molecular evolution confounds phylogenetic inference. <i>Nature Precedings</i> , 2008, , .	0.1	1
67	Regional Variation in the Density of Essential Genes in Mice. <i>PLoS Genetics</i> , 2007, 3, e72.	1.5	26
68	Evolutionary dynamics of transposable elements in the short-tailed opossum <i>Monodelphis domestica</i> . <i>Genome Research</i> , 2007, 17, 992-1004.	2.4	137
69	Dealing with uncertainty in ancestral sequence reconstruction: sampling from the posterior distribution. , 2007, , 85-94.		11
70	SINEs, evolution and genome structure in the opossum. <i>Gene</i> , 2007, 396, 46-58.	1.0	20
71	Genome of the marsupial <i>Monodelphis domestica</i> reveals innovation in non-coding sequences. <i>Nature</i> , 2007, 447, 167-177.	13.7	661
72	Comparative mitochondrial genomics of snakes: extraordinary substitution rate dynamics and functionality of the duplicate control region. <i>BMC Evolutionary Biology</i> , 2007, 7, 123.	3.2	96

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73	Coevolutionary Patterns in Cytochrome c Oxidase Subunit I Depend on Structural and Functional Context. <i>Journal of Molecular Evolution</i> , 2007, 65, 485-495.	0.8	25
74	Functionality and the evolution of marginal stability in proteins: inferences from lattice simulations. <i>Evolutionary Bioinformatics</i> , 2007, 2, 91-101.	0.6	15
75	Functionality and the Evolution of Marginal Stability in Proteins: Inferences from Lattice Simulations. <i>Evolutionary Bioinformatics</i> , 2006, 2, 117693430600200.	0.6	23
76	EGenBio: A Data Management System for Evolutionary Genomics and Biodiversity. <i>BMC Bioinformatics</i> , 2006, 7, S7.	1.2	6
77	Observations of Amino Acid Gain and Loss during Protein Evolution Are Explained by Statistical Bias. <i>Molecular Biology and Evolution</i> , 2006, 23, 1444-1449.	3.5	42
78	Assessing the Accuracy of Ancestral Protein Reconstruction Methods. <i>PLoS Computational Biology</i> , 2006, 2, e69.	1.5	187
79	SELECTIVE ADVANTAGE OF RECOMBINATION IN EVOLVING PROTEIN POPULATIONS: A LATTICE MODEL STUDY. <i>International Journal of Modern Physics C</i> , 2006, 17, 75-90.	0.8	1
80	From DNA to Fitness Differences: Sequences and Structures of Adaptive Variants of <i>Colias</i> Phosphoglucose Isomerase (PGI). <i>Molecular Biology and Evolution</i> , 2006, 23, 499-512.	3.5	77
81	Divergence, recombination and retention of functionality during protein evolution. <i>Human Genomics</i> , 2005, 2, 158.	1.4	5
82	The beetle gut: a hyperdiverse source of novel yeasts. <i>Mycological Research</i> , 2005, 109, 261-265.	2.5	259
83	Modeling protein evolution. , 2005, , .		0
84	Context Dependence and Coevolution Among Amino Acid Residues in Proteins. <i>Methods in Enzymology</i> , 2005, 395, 779-790.	0.4	28
85	Evolution of base-substitution gradients in primate mitochondrial genomes. <i>Genome Research</i> , 2005, 15, 665-673.	2.4	53
86	Assessing the Accuracy of Ancestral Protein Reconstruction Methods. <i>PLoS Computational Biology</i> , 2005, preprint, e69.	1.5	0
87	Regional variation in the density of essential genes in mice. <i>PLoS Genetics</i> , 2005, preprint, e72.	1.5	0
88	Detecting Gradients of Asymmetry in Site-Specific Substitutions in Mitochondrial Genomes. <i>DNA and Cell Biology</i> , 2004, 23, 707-714.	0.9	67
89	Estimating the Degree of Saturation in Mutant Screens. <i>Genetics</i> , 2004, 168, 489-502.	1.2	28
90	Ancestral Sequence Reconstruction in Primate Mitochondrial DNA: Compositional Bias and Effect on Functional Inference. <i>Molecular Biology and Evolution</i> , 2004, 21, 1871-1883.	3.5	66

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91	The Ambush Hypothesis: Hidden Stop Codons Prevent Off-Frame Gene Reading. DNA and Cell Biology, 2004, 23, 701-705.	0.9	119
92	Analysis of among-site variation in substitution patterns. Biological Procedures Online, 2004, 6, 180-188.	1.4	12
93	The Zuckerkandl Prize: Structure and Evolution. Journal of Molecular Evolution, 2003, 56, 375-376.	0.8	13
94	Is Sparse Taxon Sampling a Problem for Phylogenetic Inference?. Systematic Biology, 2003, 52, 124-126.	2.7	329
95	Likelihood Analysis of Asymmetrical Mutation Bias Gradients in Vertebrate Mitochondrial Genomes. Genetics, 2003, 165, 735-745.	1.2	91
96	Increased Taxon Sampling Is Advantageous for Phylogenetic Inference. Systematic Biology, 2002, 51, 664-671.	2.7	394
97	Genomic biodiversity, phylogenetics and coevolution in proteins. Applied Bioinformatics, 2002, 1, 81-92.	1.7	15
98	Evolution of functionality in lattice proteins. Journal of Molecular Graphics and Modelling, 2001, 19, 150-156.	1.3	49
99	Assessing an Unknown Evolutionary Process: Effect of Increasing Site-Specific Knowledge Through Taxon Addition. Molecular Biology and Evolution, 2000, 17, 1854-1858.	3.5	67
100	A Case for Evolutionary Genomics and the Comprehensive Examination of Sequence Biodiversity. Molecular Biology and Evolution, 2000, 17, 1776-1788.	3.5	63
101	STRUCTURES, PHYLOGENIES, AND GENOMES: THE INTEGRATED STUDY OF PROTEIN EVOLUTION. , 2000, , .		0
102	Coevolving protein residues: maximum likelihood identification and relationship to structure 1 Edited by G. Von Heijne. Journal of Molecular Biology, 1999, 287, 187-198.	2.0	242
103	Protein Evolution and Structural Genomics. , 1999, , .		0
104	Increased Accuracy in Analytical Molecular Distance Estimation. Theoretical Population Biology, 1998, 54, 78-90.	0.5	10
105	Microsatellite Behavior with Range Constraints: Parameter Estimation and Improved Distances for Use in Phylogenetic Reconstruction. Theoretical Population Biology, 1998, 53, 256-271.	0.5	47
106	Molecular Phylogeny for Colias Butterflies and Their Relatives (Lepidoptera: Pieridae). Annals of the Entomological Society of America, 1998, 91, 524-531.	1.3	35
107	Effectiveness of correlation analysis in identifying protein residues undergoing correlated evolution. Protein Engineering, Design and Selection, 1997, 10, 647-657.	1.0	120
108	Launching Microsatellites: A Review of Mutation Processes and Methods of Phylogenetic Inference. Journal of Heredity, 1997, 88, 335-342.	1.0	517

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109	Microsatellite Genetic Distances With Range Constraints: Analytic Description and Problems of Estimation. <i>Genetics</i> , 1997, 145, 207-216.	1.2	110
110	Least Squares Estimation of Molecular Distance - Noise Abatement in Phylogenetic Reconstruction. <i>Theoretical Population Biology</i> , 1994, 45, 219-226.	0.5	60