

# David D Pollock

## List of Publications by Year in descending order

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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  | Repetitive Elements May Comprise Over Two-Thirds of the Human Genome. <i>PLoS Genetics</i> , 2011, 7, e1002384.   | 1.5  | 907       |
| 2  | SARS-CoV-2 evolution during treatment of chronic infection. <i>Nature</i> , 2021, 592, 277-282.   | 13.7 | 802       |
| 3  | The genome of a songbird. <i>Nature</i> , 2010, 464, 757-762.   | 13.7 | 770       |
| 4  | Genome of the marsupial <i>Monodelphis domestica</i> reveals innovation in non-coding sequences. <i>Nature</i> , 2007, 447, 167-177.  | 13.7 | 661       |
| 5  | 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       |
| 6  | Launching Microsatellites: A Review of Mutation Processes and Methods of Phylogenetic Inference. <i>Journal of Heredity</i> , 1997, 88, 335-342.  | 1.0  | 517       |
| 7  | 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       |
| 8  | Increased Taxon Sampling Is Advantageous for Phylogenetic Inference. <i>Systematic Biology</i> , 2002, 51, 664-671.   | 2.7  | 394       |
| 9  | Is Sparse Taxon Sampling a Problem for Phylogenetic Inference?. <i>Systematic Biology</i> , 2003, 52, 124-126.  | 2.7  | 329       |
| 10 | Three crocodylian genomes reveal ancestral patterns of evolution among archosaurs. <i>Science</i> , 2014, 346, 1254449.   | 6.0  | 300       |
| 11 | 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       |
| 12 | 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       |
| 13 | 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       |
| 14 | The beetle gut: a hyperdiverse source of novel yeasts. <i>Mycological Research</i> , 2005, 109, 261-265.  | 2.5  | 259       |
| 15 | Coevolving protein residues: maximum likelihood identification and relationship to structure 1<br>1 Edited by G. Von Heijne. <i>Journal of Molecular Biology</i> , 1999, 287, 187-198.                          | 2.0  | 242       |
| 16 | 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       |
| 17 | Gene-specific RNA polymerase II phosphorylation and the CTD code. <i>Nature Structural and Molecular Biology</i> , 2010, 17, 1279-1286.   | 3.6  | 200       |
| 18 | The interface of protein structure, protein biophysics, and molecular evolution. <i>Protein Science</i> , 2012, 21, 769-785.  | 3.1  | 188       |

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|----|---|-----|-----------|
| 19 | Assessing the Accuracy of Ancestral Protein Reconstruction Methods. <i>PLoS Computational Biology</i> , 2006, 2, e69.   | 1.5 | 187       |
| 20 | 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       |
| 21 | 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       |
| 22 | LTR Retrotransposons Contribute to Genomic Gigantism in Plethodontid Salamanders. <i>Genome Biology and Evolution</i> , 2012, 4, 168-183.   | 1.1 | 152       |
| 23 | 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       |
| 24 | Effectiveness of correlation analysis in identifying protein residues undergoing correlated evolution. <i>Protein Engineering, Design and Selection</i> , 1997, 10, 647-657.  | 1.0 | 120       |
| 25 | The Ambush Hypothesis: Hidden Stop Codons Prevent Off-Frame Gene Reading. <i>DNA and Cell Biology</i> , 2004, 23, 701-705.  | 0.9 | 119       |
| 26 | 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       |
| 27 | Adaptive Evolution and Functional Redesign of Core Metabolic Proteins in Snakes. <i>PLoS ONE</i> , 2008, 3, e2201.  | 1.1 | 113       |
| 28 | Microsatellite Genetic Distances With Range Constraints: Analytic Description and Problems of Estimation. <i>Genetics</i> , 1997, 145, 207-216.   | 1.2 | 110       |
| 29 | 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        |
| 30 | 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        |
| 31 | Likelihood Analysis of Asymmetrical Mutation Bias Gradients in Vertebrate Mitochondrial Genomes. <i>Genetics</i> , 2003, 165, 735-745.  | 1.2 | 91        |
| 32 | 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        |
| 33 | A call for benchmarking transposable element annotation methods. <i>Mobile DNA</i> , 2015, 6, 13.   | 1.3 | 83        |
| 34 | 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        |
| 35 | 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        |
| 36 | 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        |

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|----|--|------|-----------|
| 37 | Assessing an Unknown Evolutionary Process: Effect of Increasing Site-Specific Knowledge Through Taxon Addition. <i>Molecular Biology and Evolution</i> , 2000, 17, 1854-1858.                  | 3.5  | 67        |
| 38 | Detecting Gradients of Asymmetry in Site-Specific Substitutions in Mitochondrial Genomes. <i>DNA and Cell Biology</i> , 2004, 23, 707-714.   | 0.9  | 67        |
| 39 | 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        |
| 40 | Nonadaptive Amino Acid Convergence Rates Decrease over Time. <i>Molecular Biology and Evolution</i> , 2015, 32, 1373-1381.   | 3.5  | 66        |
| 41 | A Case for Evolutionary Genomics and the Comprehensive Examination of Sequence Biodiversity. <i>Molecular Biology and Evolution</i> , 2000, 17, 1776-1788.                                     | 3.5  | 63        |
| 42 | Least Squares Estimation of Molecular Distance - Noise Abatement in Phylogenetic Reconstruction. <i>Theoretical Population Biology</i> , 1994, 45, 219-226.                                    | 0.5  | 60        |
| 43 | 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        |
| 44 | Evolution of base-substitution gradients in primate mitochondrial genomes. <i>Genome Research</i> , 2005, 15, 665-673.   | 2.4  | 53        |
| 45 | Identification of repeat structure in large genomes using repeat probability clouds. <i>Analytical Biochemistry</i> , 2008, 380, 77-83.  | 1.1  | 51        |
| 46 | Evolution of functionality in lattice proteins. <i>Journal of Molecular Graphics and Modelling</i> , 2001, 19, 150-156.  | 1.3  | 49        |
| 47 | Microsatellite Behavior with Range Constraints: Parameter Estimation and Improved Distances for Use in Phylogenetic Reconstruction. <i>Theoretical Population Biology</i> , 1998, 53, 256-271. | 0.5  | 47        |
| 48 | 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        |
| 49 | Amalgamated cross-species transcriptomes reveal organ-specific propensity in gene expression evolution. <i>Nature Communications</i> , 2020, 11, 4459.   | 5.8  | 46        |
| 50 | 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        |
| 51 | The tangled bank of amino acids. <i>Protein Science</i> , 2016, 25, 1354-1362.   | 3.1  | 40        |
| 52 | Molecular Phylogeny for <i>Colias</i> Butterflies and Their Relatives (Lepidoptera: Pieridae). <i>Annals of the Entomological Society of America</i> , 1998, 91, 524-531.                      | 1.3  | 35        |
| 53 | Two-pore channels for integrative Ca <sup>2+</sup> signaling. <i>Communicative and Integrative Biology</i> , 2010, 3, 12-17.   | 0.6  | 34        |
| 54 | 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        |

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|----|---|-----|-----------|
| 55 | 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        |
| 56 | 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        |
| 57 | 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        |
| 58 | Estimating the Degree of Saturation in Mutant Screens. <i>Genetics</i> , 2004, 168, 489-502.  | 1.2 | 28        |
| 59 | Context Dependence and Coevolution Among Amino Acid Residues in Proteins. <i>Methods in Enzymology</i> , 2005, 395, 779-790.  | 0.4 | 28        |
| 60 | 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        |
| 61 | 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        |
| 62 | Regional Variation in the Density of Essential Genes in Mice. <i>PLoS Genetics</i> , 2007, 3, e72.  | 1.5 | 26        |
| 63 | 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        |
| 64 | Thousands of microsatellite loci from the venomous coral snake <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        |
| 65 | 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        |
| 66 | Functionality and the Evolution of Marginal Stability in Proteins: Inferences from Lattice Simulations. <i>Evolutionary Bioinformatics</i> , 2006, 2, 117693430600200.  | 0.6 | 23        |
| 67 | 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        |
| 68 | 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        |
| 69 | 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        |
| 70 | Biliverdin Reductase B Dynamics Are Coupled to Coenzyme Binding. <i>Journal of Molecular Biology</i> , 2018, 430, 3234-3250.  | 2.0 | 22        |
| 71 | SINEs, evolution and genome structure in the opossum. <i>Gene</i> , 2007, 396, 46-58.   | 1.0 | 20        |
| 72 | Finding and extending ancient simple sequence repeat-derived regions in the human genome. <i>Mobile DNA</i> , 2020, 11, 11.   | 1.3 | 20        |

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|----|--|-----|-----------|
| 73 | 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        |
| 74 | 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        |
| 75 | Functionality and the evolution of marginal stability in proteins: inferences from lattice simulations. <i>Evolutionary Bioinformatics</i> , 2007, 2, 91-101.  | 0.6 | 15        |
| 76 | Genomic biodiversity, phylogenetics and coevolution in proteins. <i>Applied Bioinformatics</i> , 2002, 1, 81-92.   | 1.7 | 15        |
| 77 | The Zuckerkandl Prize: Structure and Evolution. <i>Journal of Molecular Evolution</i> , 2003, 56, 375-376.   | 0.8 | 13        |
| 78 | Adaptive molecular convergences. <i>Communicative and Integrative Biology</i> , 2010, 3, 67-69.  | 0.6 | 13        |
| 79 | Inference of Transposable Element Ancestry. <i>PLoS Genetics</i> , 2014, 10, e1004482.   | 1.5 | 13        |
| 80 | Analysis of among-site variation in substitution patterns. <i>Biological Procedures Online</i> , 2004, 6, 180-188.   | 1.4 | 12        |
| 81 | Dealing with uncertainty in ancestral sequence reconstruction: sampling from the posterior distribution. , 2007, , 85-94.  |     | 11        |
| 82 | Increased Accuracy in Analytical Molecular Distance Estimation. <i>Theoretical Population Biology</i> , 1998, 54, 78-90.   | 0.5 | 10        |
| 83 | Phylogenetics, likelihood, evolution and complexity. <i>Bioinformatics</i> , 2012, 28, 2989-2990.  | 1.8 | 10        |
| 84 | 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        |
| 85 | 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         |
| 86 | 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         |
| 87 | Population genomic analyses of schistosome parasites highlight critical challenges facing endgame elimination efforts. <i>Scientific Reports</i> , 2021, 11, 6884.   | 1.6 | 8         |
| 88 | EGenBio: A Data Management System for Evolutionary Genomics and Biodiversity. <i>BMC Bioinformatics</i> , 2006, 7, S7.   | 1.2 | 6         |
| 89 | Divergence, recombination and retention of functionality during protein evolution. <i>Human Genomics</i> , 2005, 2, 158.   | 1.4 | 5         |
| 90 | 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         |

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|-----|--|-----|-----------|
| 91  | Report from the First Snake Genomics and Integrative Biology Meeting. Standards in Genomic Sciences, 2012, 7, 150-152.   | 1.5 | 4         |
| 92  | Chinese alligator genome illustrates molecular adaptations. Cell Research, 2013, 23, 1254-1255.  | 5.7 | 3         |
| 93  | Mechanistic Models of Protein Evolution. , 2017, , 277-296.  |     | 3         |
| 94  | Bayesian Analysis of High-Throughput Quantitative Measurement of Protein-DNA Interactions. PLoS ONE, 2011, 6, e26105.  | 1.1 | 2         |
| 95  | SELECTIVE ADVANTAGE OF RECOMBINATION IN EVOLVING PROTEIN POPULATIONS: A LATTICE MODEL STUDY. International Journal of Modern Physics C, 2006, 17, 75-90.                       | 0.8 | 1         |
| 96  | An ancient adaptive episode of convergent molecular evolution confounds phylogenetic inference. Nature Precedings, 2008, , .   | 0.1 | 1         |
| 97  | Ancestral Sequence Reconstruction in Primate Mitochondrial DNA: Compositional Bias and Effect on Functional Inference. Molecular Biology and Evolution, 2009, 26, 481-481.     | 3.5 | 1         |
| 98  | Parallel and Convergent Molecular Evolution. , 2016, , 206-211.  |     | 1         |
| 99  | A genomic can of worms for schistosome host-specificity. Trends in Parasitology, 2022, 38, 496-497.  | 1.5 | 1         |
| 100 | Modeling protein evolution. , 2005, , .  |     | 0         |
| 101 | Identifying DNA Strands Using a Kernel of Classified Sequences. , 2009, , .  |     | 0         |
| 102 | F.44. High-throughput Parallel Pyrosequencing of T Cell Receptors from the NOD Mouse Reveals Tens of Thousands of Unique Sequences. Clinical Immunology, 2009, 131, S105-S106. | 1.4 | 0         |
| 103 | Squamate Reptile Genomics and Evolution. , 2016, , 29-49.  |     | 0         |
| 104 | Society for Molecular Biology and Evolution, Council and Business Meetings, 2017, Austin, TX. Molecular Biology and Evolution, 2018, 35, 259-261.                              | 3.5 | 0         |
| 105 | Society for Molecular Biology and Evolution, Council and Business Meetings, 2018, Yokohama, Japan. Molecular Biology and Evolution, 2019, 36, 204-206.                         | 3.5 | 0         |
| 106 | STRUCTURES, PHYLOGENIES, AND GENOMES: THE INTEGRATED STUDY OF PROTEIN EVOLUTION. , 2000, , .   |     | 0         |
| 107 | Assessing the Accuracy of Ancestral Protein Reconstruction Methods. PLoS Computational Biology, 2005, preprint, e69.   | 1.5 | 0         |
| 108 | Regional variation in the density of essential genes in mice. PLoS Genetics, 2005, preprint, e72.  | 1.5 | 0         |

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|-----|---|-----|-----------|
| 109 | Modeling Protein Evolution. Biological and Medical Physics Series, 2012, , 311-325. | 0.3 | 0         |
| 110 | Protein Evolution and Structural Genomics. , 1999, , .                              |     | 0         |