David D Pollock

List of Publications by Year
in descending order

111 papers	11,404 citations	53794 45 h-index	34986 98 g-index
128 all docs	128 docs citations	128 times ranked	15266 citing authors

#	Article	IF	Citations
1	A genomic can of worms for schistosome host-specificity. Trends in Parasitology, 2022, 38, 496-497.	3.3	1
2	Patterns of relatedness and genetic diversity inferred from whole genome sequencing of archival blood fluke miracidia (Schistosoma japonicum). PLoS Neglected Tropical Diseases, 2021, 15, e0009020.	3.0	8
3	SARS-CoV-2 evolution during treatment of chronic infection. Nature, 2021, 592, 277-282.	27.8	802
4	Population genomic analyses of schistosome parasites highlight critical challenges facing endgame elimination efforts. Scientific Reports, 2021, 11, 6884.	3.3	8
5	Selection for cooperativity causes epistasis predominately between native contacts and enables epistasis-based structure reconstruction. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	7.1	5
6	Viral CpG Deficiency Provides No Evidence That Dogs Were Intermediate Hosts for SARS-CoV-2. Molecular Biology and Evolution, 2020, 37, 2706-2710.	8.9	18
7	Amalgamated cross-species transcriptomes reveal organ-specific propensity in gene expression evolution. Nature Communications, 2020, 11, 4459.	12.8	46
8	Finding and extending ancient simple sequence repeat-derived regions in the human genome. Mobile DNA, 2020, 11, 11.	3.6	20
9	Society for Molecular Biology and Evolution, Council and Business Meetings, 2018, Yokohama, Japan. Molecular Biology and Evolution, 2019, 36, 204-206.	8.9	0
10	Society for Molecular Biology and Evolution, Council and Business Meetings, 2017, Austin, TX. Molecular Biology and Evolution, 2018, 35, 259-261.	8.9	0
11	Biliverdin Reductase B Dynamics Are Coupled to Coenzyme Binding. Journal of Molecular Biology, 2018, 430, 3234-3250.	4.2	22
12	Genome of the pitcher plant Cephalotus reveals genetic changes associated with carnivory. Nature Ecology and Evolution, 2017, 1, 59.	7.8	99
13	Sequence entropy of folding and the absolute rate of amino acid substitutions. Nature Ecology and Evolution, 2017, 1, 1923-1930.	7.8	46
14	Mechanistic Models of Protein Evolution. , 2017, , 277-296.		3
15	Whole Genome Amplification and Reduced-Representation Genome Sequencing of Schistosoma japonicum Miracidia. PLoS Neglected Tropical Diseases, 2017, 11, e0005292.	3.0	23
16	Platform technology to generate broadly crossâ€reactive antibodies to Î±â€helical epitopes in hemagglutinin proteins from influenza A viruses. Biopolymers, 2016, 106, 144-159.	2.4	10
17	The tangled bank of amino acids. Protein Science, 2016, 25, 1354-1362.	7.6	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. Genome Biology and Evolution, 2016, 8, evw013.	2.5	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. Physiological Genomics, 2015, 47, 147-157.	2.3	28
22	Nonadaptive Amino Acid Convergence Rates Decrease over Time. Molecular Biology and Evolution, 2015, 32, 1373-1381.	8.9	66
23	A call for benchmarking transposable element annotation methods. Mobile DNA, 2015, 6, 13.	3.6	83
24	Inference of Transposable Element Ancestry. PLoS Genetics, 2014, 10, e1004482.	3.5	13
25	Three crocodilian genomes reveal ancestral patterns of evolution among archosaurs. Science, 2014, 346, 1254449.	12.6	300
26	Two Antarctic penguin genomes reveal insights into their evolutionary history and molecular changes related to the Antarctic environment. GigaScience, 2014, 3, 27.	6.4	72
27	Strong evidence for protein epistasis, weak evidence against it. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, E1450-E1450.	7.1	31
28	The western painted turtle genome, a model for the evolution of extreme physiological adaptations in a slowly evolving lineage. Genome Biology, 2013, 14, R28.	9.6	276
29	The Burmese python genome reveals the molecular basis for extreme adaptation in snakes. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 20645-20650.	7.1	260
30	The king cobra genome reveals dynamic gene evolution and adaptation in the snake venom system. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 20651-20656.	7.1	412
31	Chinese alligator genome illustrates molecular adaptations. Cell Research, 2013, 23, 1254-1255.	12.0	3
32	Amino acid coevolution induces an evolutionary Stokes shift. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, E1352-9.	7.1	183
33	SP Transcription Factor Paralogs and DNA-Binding Sites Coevolve and Adaptively Converge in Mammals and Birds. Genome Biology and Evolution, 2012, 4, 1102-1117.	2.5	8
34	Germline TRAV5D-4 T-Cell Receptor Sequence Targets a Primary Insulin Peptide of NOD Mice. Diabetes, 2012, 61, 857-865.	0.6	31
35	Transcriptome sequencing of black grouse (Tetrao tetrix) for immune gene discovery and microsatellite development. Open Biology, 2012, 2, 120054.	3.6	26
36	LTR Retrotransposons Contribute to Genomic Gigantism in Plethodontid Salamanders. Genome Biology and Evolution, 2012, 4, 168-183.	2.5	152

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37	Report from the First Snake Genomics and Integrative Biology Meeting. Standards in Genomic Sciences, 2012, 7, 150-152.	1.5	4
38	Phylogenetics, likelihood, evolution and complexity. Bioinformatics, 2012, 28, 2989-2990.	4.1	10
39	Thousands of microsatellite loci from the venomous coralsnake M icrurus fulvius and variability of select loci across populations and related species. Molecular Ecology Resources, 2012, 12, 1105-1113.	4.8	26
40	Rapid Microsatellite Identification from Illumina Paired-End Genomic Sequencing in Two Birds and a Snake. PLoS ONE, 2012, 7, e30953.	2.5	208
41	The interface of protein structure, protein biophysics, and molecular evolution. Protein Science, 2012, 21, 769-785.	7.6	188
42	Modeling Protein Evolution. Biological and Medical Physics Series, 2012, , 311-325.	0.4	0
43	The genome of the green anole lizard and a comparative analysis with birds and mammals. Nature, 2011, 477, 587-591.	27.8	575
44	Sequencing the genome of the Burmese python (Python molurus bivittatus) as a model for studying extreme adaptations in snakes. Genome Biology, 2011, 12, 406.	9.6	58
45	Bayesian Analysis of High-Throughput Quantitative Measurement of Protein-DNA Interactions. PLoS ONE, 2011, 6, e26105.	2.5	2
46	Discovery of Highly Divergent Repeat Landscapes in Snake Genomes Using High-Throughput Sequencing. Genome Biology and Evolution, 2011, 3, 641-653.	2.5	87
47	A proposal to sequence the genome of a garter snake (Thamnophis sirtalis). Standards in Genomic Sciences, 2011, 4, 257-270.	1.5	31
48	A multi-organ transcriptome resource for the Burmese Python (Python molurus bivittatus). BMC Research Notes, 2011, 4, 310.	1.4	18
49	Repetitive Elements May Comprise Over Two-Thirds of the Human Genome. PLoS Genetics, 2011, 7, e1002384.	3.5	907
50	Two-pore channels for integrative Ca²⁺signaling. Communicative and Integrative Biology, 2010, 3, 12-17.	1.4	34
51	Gene-specific RNA polymerase II phosphorylation and the CTD code. Nature Structural and Molecular Biology, 2010, 17, 1279-1286.	8.2	200
52	The genome of a songbird. Nature, 2010, 464, 757-762.	27.8	770
53	Comparison of Normalization Methods for Construction of Large, Multiplex Amplicon Pools for Next-Generation Sequencing. Applied and Environmental Microbiology, 2010, 76, 3863-3868.	3.1	71
54	Rapid Likelihood Analysis on Large Phylogenies Using Partial Sampling of Substitution Histories. Molecular Biology and Evolution, 2010, 27, 249-265.	8.9	23

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55	Adaptive molecular convergences. Communicative and Integrative Biology, 2010, 3, 67-69.	1.4	13
56	Rapid identification of thousands of copperhead snake (Agkistrodon contortrix) microsatellite loci from modest amounts of 454 shotgun genome sequence. Molecular Ecology Resources, 2010, 10, 341-347.	4.8	179
57	Dynamic Nucleotide Mutation Gradients and Control Region Usage in Squamate Reptile Mitochondrial Genomes. Cytogenetic and Genome Research, 2009, 127, 112-127.	1.1	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. Molecular Biology and Evolution, 2009, 26, 481-481.	8.9	1
60	Evidence for an ancient adaptive episode of convergent molecular evolution. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 8986-8991.	7.1	284
61	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.	3.2	0
62	Intrinsic amino acid sideâ€chain hydrophilicity/hydrophobicity coefficients determined by reversedâ€phase highâ€performance liquid chromatography of model peptides: Comparison with other hydrophilicity/hydrophobicity scales. Biopolymers, 2009, 92, 573-595.	2.4	114
63	Identification of repeat structure in large genomes using repeat probability clouds. Analytical Biochemistry, 2008, 380, 77-83.	2.4	51
64	Structural, Biochemical, and in Vivo Characterization of the First Virally Encoded Cyclophilin from the Mimivirus. Journal of Molecular Biology, 2008, 378, 71-86.	4.2	30
65	Adaptive Evolution and Functional Redesign of Core Metabolic Proteins in Snakes. PLoS ONE, 2008, 3, e2201.	2.5	113
66	An ancient adaptive episode of convergent molecular evolution confounds phylogenetic inference. Nature Precedings, 2008, , .	0.1	1
67	Regional Variation in the Density of Essential Genes in Mice. PLoS Genetics, 2007, 3, e72.	3.5	26
68	Evolutionary dynamics of transposable elements in the short-tailed opossum Monodelphis domestica. Genome Research, 2007, 17, 992-1004.	5.5	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. Gene, 2007, 396, 46-58.	2.2	20
71	Genome of the marsupial Monodelphis domestica reveals innovation in non-coding sequences. Nature, 2007, 447, 167-177.	27.8	661
72	Comparative mitochondrial genomics of snakes: extraordinary substitution rate dynamics and functionality of the duplicate control region. BMC Evolutionary Biology, 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. Journal of Molecular Evolution, 2007, 65, 485-495.	1.8	25
74	Functionality and the evolution of marginal stability in proteins: inferences from lattice simulations. Evolutionary Bioinformatics, 2007, 2, 91-101.	1.2	15
75	Functionality and the Evolution of Marginal Stability in Proteins: Inferences from Lattice Simulations. Evolutionary Bioinformatics, 2006, 2, 117693430600200.	1.2	23
76	EGenBio: A Data Management System for Evolutionary Genomics and Biodiversity. BMC Bioinformatics, 2006, 7, S7.	2.6	6
77	Observations of Amino Acid Gain and Loss during Protein Evolution Are Explained by Statistical Bias. Molecular Biology and Evolution, 2006, 23, 1444-1449.	8.9	42
78	Assessing the Accuracy of Ancestral Protein Reconstruction Methods. PLoS Computational Biology, 2006, 2, e69.	3.2	187
79	SELECTIVE ADVANTAGE OF RECOMBINATION IN EVOLVING PROTEIN POPULATIONS: A LATTICE MODEL STUDY. International Journal of Modern Physics C, 2006, 17, 75-90.	1.7	1
80	From DNA to Fitness Differences: Sequences and Structures of Adaptive Variants of Colias Phosphoglucose Isomerase (PGI). Molecular Biology and Evolution, 2006, 23, 499-512.	8.9	77
81	Divergence, recombination and retention of functionality during protein evolution. Human Genomics, 2005, 2, 158.	2.9	5
82	The beetle gut: a hyperdiverse source of novel yeasts. Mycological Research, 2005, 109, 261-265.	2.5	259
83	Modeling protein evolution. , 2005, , .		0
84	Context Dependence and Coevolution Among Amino Acid Residues in Proteins. Methods in Enzymology, 2005, 395, 779-790.	1.0	28
85	Evolution of base-substitution gradients in primate mitochondrial genomes. Genome Research, 2005, 15, 665-673.	5.5	53
86	Accessing the Accuracy of Ancestral Protein Reconstruction Methods. PLoS Computational Biology, 2005, preprint, e69.	3.2	0
87	Regional variation in the density of essential genes in mice. PLoS Genetics, 2005, preprint, e72.	3.5	0
88	Detecting Gradients of Asymmetry in Site-Specific Substitutions in Mitochondrial Genomes. DNA and Cell Biology, 2004, 23, 707-714.	1.9	67
89	Estimating the Degree of Saturation in Mutant Screens. Genetics, 2004, 168, 489-502.	2.9	28
90	Ancestral Sequence Reconstruction in Primate Mitochondrial DNA: Compositional Bias and Effect on Functional Inference. Molecular Biology and Evolution, 2004, 21, 1871-1883.	8.9	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.	1.9	119
92	Analysis of among-site variation in substitution patterns. Biological Procedures Online, 2004, 6, 180-188.	2.9	12
93	Detecting Gradients of Asymmetry in Site-Specific Substitutions in Mitochondrial Genomes. DNA and Cell Biology, 2004, 23, 707-714.	1.9	0
94	The Zuckerkandl Prize: Structure and Evolution. Journal of Molecular Evolution, 2003, 56, 375-376.	1.8	13
95	Is Sparse Taxon Sampling a Problem for Phylogenetic Inference?. Systematic Biology, 2003, 52, 124-126.	5.6	329
96	Likelihood Analysis of Asymmetrical Mutation Bias Gradients in Vertebrate Mitochondrial Genomes. Genetics, 2003, 165, 735-745.	2.9	91
97	Increased Taxon Sampling Is Advantageous for Phylogenetic Inference. Systematic Biology, 2002, 51, 664-671.	5.6	394
98	Genomic biodiversity, phylogenetics and coevolution in proteins. Applied Bioinformatics, 2002, 1, 81-92.	1.6	15
99	Evolution of functionality in lattice proteins. Journal of Molecular Graphics and Modelling, 2001, 19, 150-156.	2.4	49
100	Assessing an Unknown Evolutionary Process: Effect of Increasing Site-Specific Knowledge Through Taxon Addition. Molecular Biology and Evolution, 2000, 17, 1854-1858.	8.9	67
101	A Case for Evolutionary Genomics and the Comprehensive Examination of Sequence Biodiversity. Molecular Biology and Evolution, 2000, 17, 1776-1788.	8.9	63
102	STRUCTURES, PHYLOGENIES, AND GENOMES: THE INTEGRATED STUDY OF PROTEIN EVOLUTION. , 2000, , .		0
103	Coevolving protein residues: maximum likelihood identification and relationship to structure 1 1Edited by G. Von Heijne. Journal of Molecular Biology, 1999, 287, 187-198.	4.2	242
104	Protein Evolution and Structural Genomics. , 1999, , .		0
105	Increased Accuracy in Analytical Molecular Distance Estimation. Theoretical Population Biology, 1998, 54, 78-90.	1.1	10
106	Microsatellite Behavior with Range Constraints: Parameter Estimation and Improved Distances for Use in Phylogenetic Reconstruction. Theoretical Population Biology, 1998, 53, 256-271.	1.1	47
107	Molecular Phylogeny for Colias Butterflies and Their Relatives (Lepidoptera: Pieridae). Annals of the Entomological Society of America, 1998, 91, 524-531.	2.5	35
108	Effectiveness of correlation analysis in identifying protein residues undergoing correlated evolution. Protein Engineering, Design and Selection, 1997, 10, 647-657.	2.1	120

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109	Launching Microsatellites: A Review of Mutation Processes and Methods of Phylogenetic Inference. Journal of Heredity, 1997, 88, 335-342.	2.4	517
110	Microsatellite Genetic Distances With Range Constraints: Analytic Description and Problems of Estimation. Genetics, 1997, 145, 207-216.	2.9	110
111	Least Squares Estimation of Molecular Distance - Noise Abatement in Phylogenetic Reconstruction. Theoretical Population Biology, 1994, 45, 219-226.	1.1	60