

David D Pollock

List of Publications by Year in descending order

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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	Repetitive Elements May Comprise Over Two-Thirds of the Human Genome. PLoS Genetics, 2011, 7, e1002384.	3.5	907
2	SARS-CoV-2 evolution during treatment of chronic infection. Nature, 2021, 592, 277-282.	27.8	802
3	The genome of a songbird. Nature, 2010, 464, 757-762.	27.8	770
4	Genome of the marsupial Monodelphis domestica reveals innovation in non-coding sequences. Nature, 2007, 447, 167-177.	27.8	661
5	The genome of the green anole lizard and a comparative analysis with birds and mammals. Nature, 2011, 477, 587-591.	27.8	575
6	Launching Microsatellites: A Review of Mutation Processes and Methods of Phylogenetic Inference. Journal of Heredity, 1997, 88, 335-342.	2.4	517
7	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
8	Increased Taxon Sampling Is Advantageous for Phylogenetic Inference. Systematic Biology, 2002, 51, 664-671.	5.6	394
9	Is Sparse Taxon Sampling a Problem for Phylogenetic Inference?. Systematic Biology, 2003, 52, 124-126.	5.6	329
10	Three crocodilian genomes reveal ancestral patterns of evolution among archosaurs. Science, 2014, 346, 1254449.	12.6	300
11	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
12	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
13	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
14	The beetle gut: a hyperdiverse source of novel yeasts. Mycological Research, 2005, 109, 261-265.	2.5	259
15	Coevolving protein residues: maximum likelihood identification and relationship to structure 1 Edited by G. Von Heijne. Journal of Molecular Biology, 1999, 287, 187-198.	4.2	242
16	Rapid Microsatellite Identification from Illumina Paired-End Genomic Sequencing in Two Birds and a Snake. PLoS ONE, 2012, 7, e30953.	2.5	208
17	Gene-specific RNA polymerase II phosphorylation and the CTD code. Nature Structural and Molecular Biology, 2010, 17, 1279-1286.	8.2	200
18	The interface of protein structure, protein biophysics, and molecular evolution. Protein Science, 2012, 21, 769-785.	7.6	188

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19	Assessing the Accuracy of Ancestral Protein Reconstruction Methods. PLoS Computational Biology, 2006, 2, e69.	3.2	187
20	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
21	Rapid identification of thousands of copperhead snake (<i>Agkistrodon contortrix</i>) microsatellite loci from modest amounts of 454 shotgun genome sequence. Molecular Ecology Resources, 2010, 10, 341-347.	4.8	179
22	LTR Retrotransposons Contribute to Genomic Gigantism in Plethodontid Salamanders. Genome Biology and Evolution, 2012, 4, 168-183.	2.5	152
23	Evolutionary dynamics of transposable elements in the short-tailed opossum <i>Monodelphis domestica</i> . Genome Research, 2007, 17, 992-1004.	5.5	137
24	Effectiveness of correlation analysis in identifying protein residues undergoing correlated evolution. Protein Engineering, Design and Selection, 1997, 10, 647-657.	2.1	120
25	The Ambush Hypothesis: Hidden Stop Codons Prevent Off-Frame Gene Reading. DNA and Cell Biology, 2004, 23, 701-705.	1.9	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. Biopolymers, 2009, 92, 573-595.	2.4	114
27	Adaptive Evolution and Functional Redesign of Core Metabolic Proteins in Snakes. PLoS ONE, 2008, 3, e2201.	2.5	113
28	Microsatellite Genetic Distances With Range Constraints: Analytic Description and Problems of Estimation. Genetics, 1997, 145, 207-216.	2.9	110
29	Genome of the pitcher plant <i>Cephalotus</i> reveals genetic changes associated with carnivory. Nature Ecology and Evolution, 2017, 1, 59.	7.8	99
30	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
31	Likelihood Analysis of Asymmetrical Mutation Bias Gradients in Vertebrate Mitochondrial Genomes. Genetics, 2003, 165, 735-745.	2.9	91
32	Discovery of Highly Divergent Repeat Landscapes in Snake Genomes Using High-Throughput Sequencing. Genome Biology and Evolution, 2011, 3, 641-653.	2.5	87
33	A call for benchmarking transposable element annotation methods. Mobile DNA, 2015, 6, 13.	3.6	83
34	From DNA to Fitness Differences: Sequences and Structures of Adaptive Variants of <i>Colias</i> Phosphoglucose Isomerase (PGI). Molecular Biology and Evolution, 2006, 23, 499-512.	8.9	77
35	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
36	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

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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.	8.9	67
38	Detecting Gradients of Asymmetry in Site-Specific Substitutions in Mitochondrial Genomes. <i>DNA and Cell Biology</i> , 2004, 23, 707-714.	1.9	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.	8.9	66
40	Nonadaptive Amino Acid Convergence Rates Decrease over Time. <i>Molecular Biology and Evolution</i> , 2015, 32, 1373-1381.	8.9	66
41	A Case for Evolutionary Genomics and the Comprehensive Examination of Sequence Biodiversity. <i>Molecular Biology and Evolution</i> , 2000, 17, 1776-1788.	8.9	63
42	Least Squares Estimation of Molecular Distance - Noise Abatement in Phylogenetic Reconstruction. <i>Theoretical Population Biology</i> , 1994, 45, 219-226.	1.1	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.	9.6	58
44	Evolution of base-substitution gradients in primate mitochondrial genomes. <i>Genome Research</i> , 2005, 15, 665-673.	5.5	53
45	Identification of repeat structure in large genomes using repeat probability clouds. <i>Analytical Biochemistry</i> , 2008, 380, 77-83.	2.4	51
46	Evolution of functionality in lattice proteins. <i>Journal of Molecular Graphics and Modelling</i> , 2001, 19, 150-156.	2.4	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.	1.1	47
48	Sequence entropy of folding and the absolute rate of amino acid substitutions. <i>Nature Ecology and Evolution</i> , 2017, 1, 1923-1930.	7.8	46
49	Amalgamated cross-species transcriptomes reveal organ-specific propensity in gene expression evolution. <i>Nature Communications</i> , 2020, 11, 4459.	12.8	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.	8.9	42
51	The tangled bank of amino acids. <i>Protein Science</i> , 2016, 25, 1354-1362.	7.6	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.	2.5	35
53	Two-pore channels for integrative Ca^{2+} signaling. <i>Communicative and Integrative Biology</i> , 2010, 3, 12-17.	1.4	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.	0.6	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.	7.1	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.	4.2	30
58	Estimating the Degree of Saturation in Mutant Screens. <i>Genetics</i> , 2004, 168, 489-502.	2.9	28
59	Context Dependence and Coevolution Among Amino Acid Residues in Proteins. <i>Methods in Enzymology</i> , 2005, 395, 779-790.	1.0	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.	2.3	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.	2.5	28
62	Regional Variation in the Density of Essential Genes in Mice. <i>PLoS Genetics</i> , 2007, 3, e72.	3.5	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.	3.6	26
64	Thousands of microsatellite loci from the venomous coralsnake <i>Microcerurus fulvius</i> and variability of select loci across populations and related species. <i>Molecular Ecology Resources</i> , 2012, 12, 1105-1113.	4.8	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.	1.8	25
66	Functionality and the Evolution of Marginal Stability in Proteins: Inferences from Lattice Simulations. <i>Evolutionary Bioinformatics</i> , 2006, 2, 117693430600200.	1.2	23
67	Rapid Likelihood Analysis on Large Phylogenies Using Partial Sampling of Substitution Histories. <i>Molecular Biology and Evolution</i> , 2010, 27, 249-265.	8.9	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.	3.0	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.	1.1	22
70	Biliverdin Reductase B Dynamics Are Coupled to Coenzyme Binding. <i>Journal of Molecular Biology</i> , 2018, 430, 3234-3250.	4.2	22
71	SINEs, evolution and genome structure in the opossum. <i>Gene</i> , 2007, 396, 46-58.	2.2	20
72	Finding and extending ancient simple sequence repeat-derived regions in the human genome. <i>Mobile DNA</i> , 2020, 11, 11.	3.6	20

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73	A multi-organ transcriptome resource for the Burmese Python (<i>Python molurus bivittatus</i>). BMC Research Notes, 2011, 4, 310.	1.4	18
74	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
75	Functionality and the evolution of marginal stability in proteins: inferences from lattice simulations. Evolutionary Bioinformatics, 2007, 2, 91-101.	1.2	15
76	Genomic biodiversity, phylogenetics and coevolution in proteins. Applied Bioinformatics, 2002, 1, 81-92.	1.6	15
77	The Zuckerkandl Prize: Structure and Evolution. Journal of Molecular Evolution, 2003, 56, 375-376.	1.8	13
78	Adaptive molecular convergences. Communicative and Integrative Biology, 2010, 3, 67-69.	1.4	13
79	Inference of Transposable Element Ancestry. PLoS Genetics, 2014, 10, e1004482.	3.5	13
80	Analysis of among-site variation in substitution patterns. Biological Procedures Online, 2004, 6, 180-188.	2.9	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. Theoretical Population Biology, 1998, 54, 78-90.	1.1	10
83	Phylogenetics, likelihood, evolution and complexity. Bioinformatics, 2012, 28, 2989-2990.	4.1	10
84	Platform technology to generate broadly cross-reactive antibodies to α -helical epitopes in hemagglutinin proteins from influenza A viruses. Biopolymers, 2016, 106, 144-159.	2.4	10
85	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
86	Patterns of relatedness and genetic diversity inferred from whole genome sequencing of archival blood fluke miracidia (<i>Schistosoma japonicum</i>). PLoS Neglected Tropical Diseases, 2021, 15, e0009020.	3.0	8
87	Population genomic analyses of schistosome parasites highlight critical challenges facing endgame elimination efforts. Scientific Reports, 2021, 11, 6884.	3.3	8
88	EGenBio: A Data Management System for Evolutionary Genomics and Biodiversity. BMC Bioinformatics, 2006, 7, S7.	2.6	6
89	Divergence, recombination and retention of functionality during protein evolution. Human Genomics, 2005, 2, 158.	2.9	5
90	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

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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.	12.0	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.	2.5	2
95	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
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.	8.9	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.	3.3	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.	3.2	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.	8.9	0
105	Society for Molecular Biology and Evolution, Council and Business Meetings, 2018, Yokohama, Japan. Molecular Biology and Evolution, 2019, 36, 204-206.	8.9	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.	3.2	0
108	Regional variation in the density of essential genes in mice. PLoS Genetics, 2005, preprint, e72.	3.5	0

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109	Modeling Protein Evolution. Biological and Medical Physics Series, 2012, , 311-325.	0.4	0
110	Protein Evolution and Structural Genomics. , 1999, , .		0
111	Detecting Gradients of Asymmetry in Site-Specific Substitutions in Mitochondrial Genomes. DNA and Cell Biology, 2004, 23, 707-714.	1.9	0