Adam C Siepel

List of Publications by Year
in descending order

105 papers	28,684 citations	38742 50 h-index	31849 101 g-index
134 all docs	134 docs citations	134 times ranked	36781 citing authors

#	Article	IF	Citations
1	A Deep-Learning Approach for Inference of Selective Sweeps from the Ancestral Recombination Graph. Molecular Biology and Evolution, 2022, 39, .	8.9	27
2	A multiple alignment workflow shows the effect of repeat masking and parameter tuning on alignment in plants. Plant Genome, 2022, 15, e20204.	2.8	5
3	Deconvolution of expression for nascent RNA-sequencing data (DENR) highlights pre-RNA isoform diversity in human cells. Bioinformatics, 2021, 37, 4727-4736.	4.1	4
4	Characterizing RNA stability genome-wide through combined analysis of PRO-seq and RNA-seq data. BMC Biology, 2021, 19, 30.	3.8	38
5	ACE: a probabilistic model for characterizing gene-level essentiality in CRISPR screens. Genome Biology, 2021, 22, 278.	8.8	3
6	Mapping gene flow between ancient hominins through demography-aware inference of the ancestral recombination graph. PLoS Genetics, 2020, 16, e1008895.	3.5	76
7	Phylogenetic Modeling of Regulatory Element Turnover Based on Epigenomic Data. Molecular Biology and Evolution, 2020, 37, 2137-2152.	8.9	14
8	An inferred fitness consequence map of the rice genome. Nature Plants, 2020, 6, 119-130.	9.3	20
9	From Summary Statistics to Gene Trees: Methods for Inferring Positive Selection. Trends in Genetics, 2020, 36, 243-258.	6.7	28
10	Inference of Ancestral Recombination Graphs Using ARGweaver. Methods in Molecular Biology, 2020, 2090, 231-266.	0.9	27
11	Genomic islands of differentiation in a rapid avian radiation have been driven by recent selective sweeps. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 30554-30565.	7.1	40
12	A community-maintained standard library of population genetic models. ELife, 2020, 9, .	6.0	112
13	Challenges in funding and developing genomic software: roots and remedies. Genome Biology, 2019, 20, 147.	8.8	21
14	Estimation of allele-specific fitness effects across human protein-coding sequences and implications for disease. Genome Research, 2019, 29, 1310-1321.	5.5	24
15	An evolutionary framework for measuring epigenomic information and estimating cell-type-specific fitness consequences. Nature Genetics, 2019, 51, 335-342.	21.4	33
16	PhastWeb: a web interface for evolutionary conservation scoring of multiple sequence alignments using phastCons and phyloP. Bioinformatics, 2019, 35, 2320-2322.	4.1	44
17	Scikit-ribo Enables Accurate Estimation and Robust Modeling of Translation Dynamics at Codon Resolution. Cell Systems, 2018, 6, 180-191.e4.	6.2	41
18	Dynamic evolution of regulatory element ensembles in primate CD4+ T cells. Nature Ecology and Evolution, 2018, 2, 537-548.	7.8	65

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19	Deep experimental profiling of microRNA diversity, deployment, and evolution across the *Drosophila* genus. Genome Research, 2018, 28, 52-65.	5.5	39
20	Fast, scalable prediction of deleterious noncoding variants from functional and population genomic data. Nature Genetics, 2017, 49, 618-624.	21.4	299
21	Is a super-enhancer greater than the sum of its parts?. Nature Genetics, 2017, 49, 2-3.	21.4	70
22	Nascent RNA sequencing reveals a dynamic global transcriptional response at genes and enhancers to the natural medicinal compound celastrol. Genome Research, 2017, 27, 1816-1829.	5.5	31
23	New genes often acquire male-specific functions but rarely become essential in *Drosophila*. Genes and Development, 2017, 31, 1841-1846.	5.9	71
24	Ancient gene flow from early modern humans into Eastern Neanderthals. Nature, 2016, 530, 429-433.	27.8	392
25	Demographically-Based Evaluation of Genomic Regions under Selection in Domestic Dogs. PLoS Genetics, 2016, 12, e1005851.	3.5	77
26	Distinguishing noise from signal in patterns of genomic divergence in a highly polymorphic avian radiation. Molecular Ecology, 2015, 24, 4238-4251.	3.9	72
27	A method for calculating probabilities of fitness consequences for point mutations across the human genome. Nature Genetics, 2015, 47, 276-283.	21.4	247
28	GAGA Factor Maintains Nucleosome-Free Regions and Has a Role in RNA Polymerase II Recruitment to Promoters. PLoS Genetics, 2015, 11, e1005108.	3.5	87
29	Identification of active transcriptional regulatory elements from GRO-seq data. Nature Methods, 2015, 12, 433-438.	19.0	198
30	Genome-Wide Inference of Ancestral Recombination Graphs. PLoS Genetics, 2014, 10, e1004342.	3.5	323
31	Genome Sequencing Highlights the Dynamic Early History of Dogs. PLoS Genetics, 2014, 10, e1004016.	3.5	481
32	The draft genome sequence of the ferret (Mustela putorius furo) facilitates study of human respiratory disease. Nature Biotechnology, 2014, 32, 1250-1255.	17.5	110
33	Enabling large-scale next-generation sequence assembly with Blacklight. Concurrency Computation Practice and Experience, 2014, 26, 2157-2166.	2.2	8
34	Diversity of miRNAs, siRNAs, and piRNAs across 25 *Drosophila* cell lines. Genome Research, 2014, 24, 1236-1250.	5.5	66
35	Contrasting X-Linked and Autosomal Diversity across 14 Human Populations. American Journal of Human Genetics, 2014, 94, 827-844.	6.2	61
36	Analysis of nascent RNA identifies a unified architecture of initiation regions at mammalian promoters and enhancers. Nature Genetics, 2014, 46, 1311-1320.	21.4	572

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37	Diverse modes of evolutionary emergence and flux of conserved microRNA clusters. Rna, 2014, 20, 1850-1863.	3.5	40
38	Cis-regulatory elements and human evolution. Current Opinion in Genetics and Development, 2014, 29, 81-89.	3.3	51
39	Adaptive evolution of testis-specific, recently evolved, clustered miRNAs in *Drosophila*. Rna, 2014, 20, 1195-1209.	3.5	47
40	Evolutionary and Population Genomics of the Cavity Causing Bacteria Streptococcus mutans. Molecular Biology and Evolution, 2013, 30, 881-893.	8.9	168
41	The impact of age, biogenesis, and genomic clustering on *Drosophila* microRNA evolution. Rna, 2013, 19, 1295-1308.	3.5	35
42	Signaling Pathways Differentially Affect RNA Polymerase II Initiation, Pausing, and Elongation Rate in Cells. Molecular Cell, 2013, 50, 212-222.	9.7	300
43	Genome-wide inference of natural selection on human transcription factor binding sites. Nature Genetics, 2013, 45, 723-729.	21.4	121
44	A Model-Based Analysis of GC-Biased Gene Conversion in the Human and Chimpanzee Genomes. PLoS Genetics, 2013, 9, e1003684.	3.5	74
45	Inference of Natural Selection from Interspersed Genomic Elements Based on Polymorphism and Divergence. Molecular Biology and Evolution, 2013, 30, 1159-1171.	8.9	77
46	Gene Regulation by CcpA and Catabolite Repression Explored by RNA-Seq in Streptococcus mutans. PLoS ONE, 2013, 8, e60465.	2.5	74
47	Population Genomic Analysis Reveals a Rich Speciation and Demographic History of Orang-utans (Pongo pygmaeus and Pongo abelii). PLoS ONE, 2013, 8, e77175.	2.5	23
48	Accurate Prediction of Inducible Transcription Factor Binding Intensities In Vivo. PLoS Genetics, 2012, 8, e1002610.	3.5	56
49	The Role of GC-Biased Gene Conversion in Shaping the Fastest Evolving Regions of the Human Genome. Molecular Biology and Evolution, 2012, 29, 1047-1057.	8.9	86
50	Replacing and Additive Horizontal Gene Transfer in Streptococcus. Molecular Biology and Evolution, 2012, 29, 3309-3320.	8.9	33
51	Three Periods of Regulatory Innovation During Vertebrate Evolution. Science, 2011, 333, 1019-1024.	12.6	127
52	A Rapid, Extensive, and Transient Transcriptional Response to Estrogen Signaling in Breast Cancer Cells. Cell, 2011, 145, 622-634.	28.9	458
53	Bayesian inference of ancient human demography from individual genome sequences. Nature Genetics, 2011, 43, 1031-1034.	21.4	526
54	Error and Error Mitigation in Low-Coverage Genome Assemblies. PLoS ONE, 2011, 6, e17034.	2.5	33

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55	Comparative Genomic Analysis of the Streptococcus dysgalactiae Species Group: Gene Content, Molecular Adaptation, and Promoter Evolution. Genome Biology and Evolution, 2011, 3, 168-185.	2.5	52
56	Comparative and demographic analysis of orang-utan genomes. Nature, 2011, 469, 529-533.	27.8	541
57	A high-resolution map of human evolutionary constraint using 29 mammals. Nature, 2011, 478, 476-482.	27.8	1,016
58	PHAST and RPHAST: phylogenetic analysis with space/time models. Briefings in Bioinformatics, 2011, 12, 41-51.	6.5	396
59	Analyses of X-linked and autosomal genetic variation in population-scale whole genome sequencing. Nature Genetics, 2011, 43, 741-743.	21.4	81
60	Widespread regulatory activity of vertebrate microRNA* species. Rna, 2011, 17, 312-326.	3.5	293
61	Positive selection on apoptosis related genes. FEBS Letters, 2010, 584, 469-476.	2.8	38
62	Detection of nonneutral substitution rates on mammalian phylogenies. Genome Research, 2010, 20, 110-121.	5.5	1,878
63	Reconstructing Histories of Complex Gene Clusters on a Phylogeny. Journal of Computational Biology, 2010, 17, 1267-1279.	1.6	8
64	A Simple Genetic Architecture Underlies Morphological Variation in Dogs. PLoS Biology, 2010, 8, e1000451.	5.6	429
65	The completion of the Mammalian Gene Collection (MGC). Genome Research, 2009, 19, 2324-2333.	5.5	125
66	Evolutionary History Reconstruction for Mammalian Complex Gene Clusters. Journal of Computational Biology, 2009, 16, 1051-1070.	1.6	7
67	Darwinian alchemy: Human genes from noncoding DNA. Genome Research, 2009, 19, 1693-1695.	5.5	66
68	Phylogenomics of primates and their ancestral populations. Genome Research, 2009, 19, 1929-1941.	5.5	53
69	Reconstructing Histories of Complex Gene Clusters on a Phylogeny. Lecture Notes in Computer Science, 2009, , 150-163.	1.3	2
70	Sequencing and Comparative Analysis of a Conserved Syntenic Segment in the Solanaceae. Genetics, 2008, 180, 391-408.	2.9	105
71	Accelerated sequence divergence of conserved genomic elements in Drosophila melanogaster. Genome Research, 2008, 18, 1592-1601.	5.5	23
72	Patterns of Positive Selection in Six Mammalian Genomes. PLoS Genetics, 2008, 4, e1000144.	3.5	529

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73	Reconstructing the Evolutionary History of Complex Human Gene Clusters. , 2008, , 29-49.		9
74	Genomic Analyses of Transcription Factor Binding, Histone Acetylation, and Gene Expression Reveal Mechanistically Distinct Classes of Estrogen-Regulated Promoters. Molecular and Cellular Biology, 2007, 27, 5090-5104.	2.3	178
75	Targeted discovery of novel human exons by comparative genomics. Genome Research, 2007, 17, 1763-1773.	5.5	42
76	28-Way vertebrate alignment and conservation track in the UCSC Genome Browser. Genome Research, 2007, 17, 1797-1808.	5.5	237
77	Evolutionary and Biomedical Insights from the Rhesus Macaque Genome. Science, 2007, 316, 222-234.	12.6	1,283
78	Analyses of deep mammalian sequence alignments and constraint predictions for 1% of the human genome. Genome Research, 2007, 17, 760-774.	5.5	184
79	Identification and analysis of functional elements in 1% of the human genome by the ENCODE pilot project. Nature, 2007, 447, 799-816.	27.8	4,709
80	A distal enhancer and an ultraconserved exon are derived from a novel retroposon. Nature, 2006, 441, 87-90.	27.8	452
81	An RNA gene expressed during cortical development evolved rapidly in humans. Nature, 2006, 443, 167-172.	27.8	884
82	Identification and Classification of Conserved RNA Secondary Structures in the Human Genome. PLoS Computational Biology, 2006, 2, e33.	3.2	439
83	Forces Shaping the Fastest Evolving Regions in the Human Genome. PLoS Genetics, 2006, 2, e168.	3.5	399
84	New Methods for Detecting Lineage-Specific Selection. Lecture Notes in Computer Science, 2006, , 190-205.	1.3	158
85	Computational screening of conserved genomic DNA in search of functional noncoding elements. Nature Methods, 2005, 2, 535-545.	19.0	52
86	Evolutionarily conserved elements in vertebrate, insect, worm, and yeast genomes. Genome Research, 2005, 15, 1034-1050.	5.5	3,517
87	Phylogenetic Hidden Markov Models. , 2005, , 325-351.		78
88	Computational identification of evolutionarily conserved exons. , 2004, , .		56
89	Combining Phylogenetic and Hidden Markov Models in Biosequence Analysis. Journal of Computational Biology, 2004, 11, 413-428.	1.6	207
90	Efficient approximations for learning phylogenetic HMM models from data. Bioinformatics, 2004, 20, i161-i168.	4.1	27

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91	Sequence and comparative analysis of the chicken genome provide unique perspectives on vertebrate evolution. Nature, 2004, 432, 695-716.	27.8	2,421
92	Comparative analyses of multi-species sequences from targeted genomic regions. Nature, 2003, 424, 788-793.	27.8	584
93	An Algorithm to Enumerate Sorting Reversals for Signed Permutations. Journal of Computational Biology, 2003, 10, 575-597.	1.6	31
94	Phylogenetic Estimation of Context-Dependent Substitution Rates by Maximum Likelihood. Molecular Biology and Evolution, 2003, 21, 468-488.	8.9	351
95	Combining phylogenetic and hidden Markov models in biosequence analysis. , 2003, , .		29
96	An algorithm to enumerate all sorting reversals. , 2002, , .		20
97	A simplified hillslope erosion model with vegetation elements for practical applications. Journal of Hydrology, 2002, 258, 111-121.	5.4	47
98	Inversion Medians Outperform Breakpoint Medians in Phylogeny Reconstruction from Gene-Order Data. Lecture Notes in Computer Science, 2002, , 521-536.	1.3	51
99	An integration platform for heterogeneous bioinformatics software components. IBM Systems Journal, 2001, 40, 570-591.	3.0	32
100	Bioinformatics for Rice Resources. Novartis Foundation Symposium, 2001, 236, 59-84.	1.1	2
101	Finding an Optimal Inversion Median: Experimental Results. Lecture Notes in Computer Science, 2001, , 189-203.	1.3	40
102	The Genome Sequence DataBase: towards an integrated functional genomics resource. Nucleic Acids Research, 1999, 27, 35-38.	14.5	26
103	The Genome Sequence DataBase (GSDB): improving data quality and data access. Nucleic Acids Research, 1998, 26, 21-26.	14.5	19
104	The Genome Sequence DataBase version 1.0 (GSDB): from low pass sequences to complete genomes. Nucleic Acids Research, 1997, 25, 18-23.	14.5	15
105	A Computer Program Designed to Screen Rapidly for HIV Type 1 Intersubtype Recombinant Sequences. AIDS Research and Human Retroviruses, 1995, 11, 1413-1416.	1.1	232