

# Adam C Siepel

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/4099094/publications.pdf>

Version: 2024-02-01

105  
papers

28,684  
citations

44444

50  
h-index

36203

101  
g-index

134  
all docs

134  
docs citations

134  
times ranked

41325  
citing authors

#	ARTICLE	IF	CITATIONS
1	Identification and analysis of functional elements in 1% of the human genome by the ENCODE pilot project. <i>Nature</i> , 2007, 447, 799-816.	13.7	4,709
2	Evolutionarily conserved elements in vertebrate, insect, worm, and yeast genomes. <i>Genome Research</i> , 2005, 15, 1034-1050.	2.4	3,517
3	Sequence and comparative analysis of the chicken genome provide unique perspectives on vertebrate evolution. <i>Nature</i> , 2004, 432, 695-716.	13.7	2,421
4	Detection of nonneutral substitution rates on mammalian phylogenies. <i>Genome Research</i> , 2010, 20, 110-121.	2.4	1,878
5	Evolutionary and Biomedical Insights from the Rhesus Macaque Genome. <i>Science</i> , 2007, 316, 222-234.	6.0	1,283
6	A high-resolution map of human evolutionary constraint using 29 mammals. <i>Nature</i> , 2011, 478, 476-482.	13.7	1,016
7	An RNA gene expressed during cortical development evolved rapidly in humans. <i>Nature</i> , 2006, 443, 167-172.	13.7	884
8	Comparative analyses of multi-species sequences from targeted genomic regions. <i>Nature</i> , 2003, 424, 788-793.	13.7	584
9	Analysis of nascent RNA identifies a unified architecture of initiation regions at mammalian promoters and enhancers. <i>Nature Genetics</i> , 2014, 46, 1311-1320.	9.4	572
10	Comparative and demographic analysis of orang-utan genomes. <i>Nature</i> , 2011, 469, 529-533.	13.7	541
11	Patterns of Positive Selection in Six Mammalian Genomes. <i>PLoS Genetics</i> , 2008, 4, e1000144.	1.5	529
12	Bayesian inference of ancient human demography from individual genome sequences. <i>Nature Genetics</i> , 2011, 43, 1031-1034.	9.4	526
13	Genome Sequencing Highlights the Dynamic Early History of Dogs. <i>PLoS Genetics</i> , 2014, 10, e1004016.	1.5	481
14	A Rapid, Extensive, and Transient Transcriptional Response to Estrogen Signaling in Breast Cancer Cells. <i>Cell</i> , 2011, 145, 622-634.	13.5	458
15	A distal enhancer and an ultraconserved exon are derived from a novel retroposon. <i>Nature</i> , 2006, 441, 87-90.	13.7	452
16	Identification and Classification of Conserved RNA Secondary Structures in the Human Genome. <i>PLoS Computational Biology</i> , 2006, 2, e33.	1.5	439
17	A Simple Genetic Architecture Underlies Morphological Variation in Dogs. <i>PLoS Biology</i> , 2010, 8, e1000451.	2.6	429
18	Forces Shaping the Fastest Evolving Regions in the Human Genome. <i>PLoS Genetics</i> , 2006, 2, e168.	1.5	399

#	ARTICLE	IF	CITATIONS
19	PHAST and RPHAST: phylogenetic analysis with space/time models. <i>Briefings in Bioinformatics</i> , 2011, 12, 41-51.	3.2	396
20	Ancient gene flow from early modern humans into Eastern Neanderthals. <i>Nature</i> , 2016, 530, 429-433.	13.7	392
21	Phylogenetic Estimation of Context-Dependent Substitution Rates by Maximum Likelihood. <i>Molecular Biology and Evolution</i> , 2003, 21, 468-488.	3.5	351
22	Genome-Wide Inference of Ancestral Recombination Graphs. <i>PLoS Genetics</i> , 2014, 10, e1004342.	1.5	323
23	Signaling Pathways Differentially Affect RNA Polymerase II Initiation, Pausing, and Elongation Rate in Cells. <i>Molecular Cell</i> , 2013, 50, 212-222.	4.5	300
24	Fast, scalable prediction of deleterious noncoding variants from functional and population genomic data. <i>Nature Genetics</i> , 2017, 49, 618-624.	9.4	299
25	Widespread regulatory activity of vertebrate microRNA* species. <i>Rna</i> , 2011, 17, 312-326.	1.6	293
26	A method for calculating probabilities of fitness consequences for point mutations across the human genome. <i>Nature Genetics</i> , 2015, 47, 276-283.	9.4	247
27	28-Way vertebrate alignment and conservation track in the UCSC Genome Browser. <i>Genome Research</i> , 2007, 17, 1797-1808.	2.4	237
28	A Computer Program Designed to Screen Rapidly for HIV Type 1 Intersubtype Recombinant Sequences. <i>AIDS Research and Human Retroviruses</i> , 1995, 11, 1413-1416.	0.5	232
29	Combining Phylogenetic and Hidden Markov Models in Biosequence Analysis. <i>Journal of Computational Biology</i> , 2004, 11, 413-428.	0.8	207
30	Identification of active transcriptional regulatory elements from GRO-seq data. <i>Nature Methods</i> , 2015, 12, 433-438.	9.0	198
31	Analyses of deep mammalian sequence alignments and constraint predictions for 1% of the human genome. <i>Genome Research</i> , 2007, 17, 760-774.	2.4	184
32	Genomic Analyses of Transcription Factor Binding, Histone Acetylation, and Gene Expression Reveal Mechanistically Distinct Classes of Estrogen-Regulated Promoters. <i>Molecular and Cellular Biology</i> , 2007, 27, 5090-5104.	1.1	178
33	Evolutionary and Population Genomics of the Cavity Causing Bacteria <i>Streptococcus mutans</i> . <i>Molecular Biology and Evolution</i> , 2013, 30, 881-893.	3.5	168
34	New Methods for Detecting Lineage-Specific Selection. <i>Lecture Notes in Computer Science</i> , 2006, , 190-205.	1.0	158
35	Three Periods of Regulatory Innovation During Vertebrate Evolution. <i>Science</i> , 2011, 333, 1019-1024.	6.0	127
36	The completion of the Mammalian Gene Collection (MGC). <i>Genome Research</i> , 2009, 19, 2324-2333.	2.4	125

#	ARTICLE	IF	CITATIONS
37	Genome-wide inference of natural selection on human transcription factor binding sites. <i>Nature Genetics</i> , 2013, 45, 723-729.	9.4	121
38	A community-maintained standard library of population genetic models. <i>ELife</i> , 2020, 9, .	2.8	112
39	The draft genome sequence of the ferret ( <i>Mustela putorius furo</i> ) facilitates study of human respiratory disease. <i>Nature Biotechnology</i> , 2014, 32, 1250-1255.	9.4	110
40	Sequencing and Comparative Analysis of a Conserved Syntenic Segment in the Solanaceae. <i>Genetics</i> , 2008, 180, 391-408.	1.2	105
41	GAGA Factor Maintains Nucleosome-Free Regions and Has a Role in RNA Polymerase II Recruitment to Promoters. <i>PLoS Genetics</i> , 2015, 11, e1005108.	1.5	87
42	The Role of GC-Biased Gene Conversion in Shaping the Fastest Evolving Regions of the Human Genome. <i>Molecular Biology and Evolution</i> , 2012, 29, 1047-1057.	3.5	86
43	Analyses of X-linked and autosomal genetic variation in population-scale whole genome sequencing. <i>Nature Genetics</i> , 2011, 43, 741-743.	9.4	81
44	Phylogenetic Hidden Markov Models. , 2005, , 325-351.		78
45	Inference of Natural Selection from Interspersed Genomic Elements Based on Polymorphism and Divergence. <i>Molecular Biology and Evolution</i> , 2013, 30, 1159-1171.	3.5	77
46	Demographically-Based Evaluation of Genomic Regions under Selection in Domestic Dogs. <i>PLoS Genetics</i> , 2016, 12, e1005851.	1.5	77
47	Mapping gene flow between ancient hominins through demography-aware inference of the ancestral recombination graph. <i>PLoS Genetics</i> , 2020, 16, e1008895.	1.5	76
48	A Model-Based Analysis of GC-Biased Gene Conversion in the Human and Chimpanzee Genomes. <i>PLoS Genetics</i> , 2013, 9, e1003684.	1.5	74
49	Gene Regulation by CcpA and Catabolite Repression Explored by RNA-Seq in <i>Streptococcus mutans</i> . <i>PLoS ONE</i> , 2013, 8, e60465.	1.1	74
50	Distinguishing noise from signal in patterns of genomic divergence in a highly polymorphic avian radiation. <i>Molecular Ecology</i> , 2015, 24, 4238-4251.	2.0	72
51	New genes often acquire male-specific functions but rarely become essential in <i>Drosophila</i> . <i>Genes and Development</i> , 2017, 31, 1841-1846.	2.7	71
52	Is a super-enhancer greater than the sum of its parts?. <i>Nature Genetics</i> , 2017, 49, 2-3.	9.4	70
53	Darwinian alchemy: Human genes from noncoding DNA. <i>Genome Research</i> , 2009, 19, 1693-1695.	2.4	66
54	Diversity of miRNAs, siRNAs, and piRNAs across 25 <i>Drosophila</i> cell lines. <i>Genome Research</i> , 2014, 24, 1236-1250.	2.4	66

#	ARTICLE	IF	CITATIONS
55	Dynamic evolution of regulatory element ensembles in primate CD4+ T cells. <i>Nature Ecology and Evolution</i> , 2018, 2, 537-548.	3.4	65
56	Contrasting X-Linked and Autosomal Diversity across 14 Human Populations. <i>American Journal of Human Genetics</i> , 2014, 94, 827-844.	2.6	61
57	Computational identification of evolutionarily conserved exons. , 2004, , .		56
58	Accurate Prediction of Inducible Transcription Factor Binding Intensities In Vivo. <i>PLoS Genetics</i> , 2012, 8, e1002610.	1.5	56
59	Phylogenomics of primates and their ancestral populations. <i>Genome Research</i> , 2009, 19, 1929-1941.	2.4	53
60	Computational screening of conserved genomic DNA in search of functional noncoding elements. <i>Nature Methods</i> , 2005, 2, 535-545.	9.0	52
61	Comparative Genomic Analysis of the <i>Streptococcus dysgalactiae</i> Species Group: Gene Content, Molecular Adaptation, and Promoter Evolution. <i>Genome Biology and Evolution</i> , 2011, 3, 168-185.	1.1	52
62	Cis-regulatory elements and human evolution. <i>Current Opinion in Genetics and Development</i> , 2014, 29, 81-89.	1.5	51
63	Inversion Medians Outperform Breakpoint Medians in Phylogeny Reconstruction from Gene-Order Data. <i>Lecture Notes in Computer Science</i> , 2002, , 521-536.	1.0	51
64	A simplified hillslope erosion model with vegetation elements for practical applications. <i>Journal of Hydrology</i> , 2002, 258, 111-121.	2.3	47
65	Adaptive evolution of testis-specific, recently evolved, clustered miRNAs in <i>Drosophila</i> . <i>Rna</i> , 2014, 20, 1195-1209.	1.6	47
66	PhastWeb: a web interface for evolutionary conservation scoring of multiple sequence alignments using phastCons and phyloP. <i>Bioinformatics</i> , 2019, 35, 2320-2322.	1.8	44
67	Targeted discovery of novel human exons by comparative genomics. <i>Genome Research</i> , 2007, 17, 1763-1773.	2.4	42
68	Scikit-ribo Enables Accurate Estimation and Robust Modeling of Translation Dynamics at Codon Resolution. <i>Cell Systems</i> , 2018, 6, 180-191.e4.	2.9	41
69	Diverse modes of evolutionary emergence and flux of conserved microRNA clusters. <i>Rna</i> , 2014, 20, 1850-1863.	1.6	40
70	Finding an Optimal Inversion Median: Experimental Results. <i>Lecture Notes in Computer Science</i> , 2001, , 189-203.	1.0	40
71	Genomic islands of differentiation in a rapid avian radiation have been driven by recent selective sweeps. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 30554-30565.	3.3	40
72	Deep experimental profiling of microRNA diversity, deployment, and evolution across the <i>Drosophila</i> genus. <i>Genome Research</i> , 2018, 28, 52-65.	2.4	39

#	ARTICLE	IF	CITATIONS
73	Positive selection on apoptosis related genes. FEBS Letters, 2010, 584, 469-476.	1.3	38
74	Characterizing RNA stability genome-wide through combined analysis of PRO-seq and RNA-seq data. BMC Biology, 2021, 19, 30.	1.7	38
75	The impact of age, biogenesis, and genomic clustering on <i>Drosophila</i> microRNA evolution. Rna, 2013, 19, 1295-1308.	1.6	35
76	Error and Error Mitigation in Low-Coverage Genome Assemblies. PLoS ONE, 2011, 6, e17034.	1.1	33
77	Replacing and Additive Horizontal Gene Transfer in Streptococcus. Molecular Biology and Evolution, 2012, 29, 3309-3320.	3.5	33
78	An evolutionary framework for measuring epigenomic information and estimating cell-type-specific fitness consequences. Nature Genetics, 2019, 51, 335-342.	9.4	33
79	An integration platform for heterogeneous bioinformatics software components. IBM Systems Journal, 2001, 40, 570-591.	3.1	32
80	An Algorithm to Enumerate Sorting Reversals for Signed Permutations. Journal of Computational Biology, 2003, 10, 575-597.	0.8	31
81	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.	2.4	31
82	Combining phylogenetic and hidden Markov models in biosequence analysis. , 2003, , .		29
83	From Summary Statistics to Gene Trees: Methods for Inferring Positive Selection. Trends in Genetics, 2020, 36, 243-258.	2.9	28
84	Efficient approximations for learning phylogenetic HMM models from data. Bioinformatics, 2004, 20, i161-i168.	1.8	27
85	Inference of Ancestral Recombination Graphs Using ARGweaver. Methods in Molecular Biology, 2020, 2090, 231-266.	0.4	27
86	A Deep-Learning Approach for Inference of Selective Sweeps from the Ancestral Recombination Graph. Molecular Biology and Evolution, 2022, 39, .	3.5	27
87	The Genome Sequence DataBase: towards an integrated functional genomics resource. Nucleic Acids Research, 1999, 27, 35-38.	6.5	26
88	Estimation of allele-specific fitness effects across human protein-coding sequences and implications for disease. Genome Research, 2019, 29, 1310-1321.	2.4	24
89	Accelerated sequence divergence of conserved genomic elements in <i>Drosophila melanogaster</i> . Genome Research, 2008, 18, 1592-1601.	2.4	23
90	Population Genomic Analysis Reveals a Rich Speciation and Demographic History of Orang-utans ( <i>Pongo pygmaeus</i> and <i>Pongo abelii</i> ). PLoS ONE, 2013, 8, e77175.	1.1	23

#	ARTICLE	IF	CITATIONS
91	Challenges in funding and developing genomic software: roots and remedies. <i>Genome Biology</i> , 2019, 20, 147.	3.8	21
92	An algorithm to enumerate all sorting reversals. , 2002, , .		20
93	An inferred fitness consequence map of the rice genome. <i>Nature Plants</i> , 2020, 6, 119-130.	4.7	20
94	The Genome Sequence DataBase (GSDB): improving data quality and data access. <i>Nucleic Acids Research</i> , 1998, 26, 21-26.	6.5	19
95	The Genome Sequence DataBase version 1.0 (GSDB): from low pass sequences to complete genomes. <i>Nucleic Acids Research</i> , 1997, 25, 18-23.	6.5	15
96	Phylogenetic Modeling of Regulatory Element Turnover Based on Epigenomic Data. <i>Molecular Biology and Evolution</i> , 2020, 37, 2137-2152.	3.5	14
97	Reconstructing the Evolutionary History of Complex Human Gene Clusters. , 2008, , 29-49.		9
98	Reconstructing Histories of Complex Gene Clusters on a Phylogeny. <i>Journal of Computational Biology</i> , 2010, 17, 1267-1279.	0.8	8
99	Enabling large-scale next-generation sequence assembly with Blacklight. <i>Concurrency Computation Practice and Experience</i> , 2014, 26, 2157-2166.	1.4	8
100	Evolutionary History Reconstruction for Mammalian Complex Gene Clusters. <i>Journal of Computational Biology</i> , 2009, 16, 1051-1070.	0.8	7
101	A multiple alignment workflow shows the effect of repeat masking and parameter tuning on alignment in plants. <i>Plant Genome</i> , 2022, 15, e20204.	1.6	5
102	Deconvolution of expression for nascent RNA-sequencing data (DENR) highlights pre-RNA isoform diversity in human cells. <i>Bioinformatics</i> , 2021, 37, 4727-4736.	1.8	4
103	ACE: a probabilistic model for characterizing gene-level essentiality in CRISPR screens. <i>Genome Biology</i> , 2021, 22, 278.	3.8	3
104	Bioinformatics for Rice Resources. <i>Novartis Foundation Symposium</i> , 2001, 236, 59-84.	1.2	2
105	Reconstructing Histories of Complex Gene Clusters on a Phylogeny. <i>Lecture Notes in Computer Science</i> , 2009, , 150-163.	1.0	2