

# Adam C Siepel

## List of Publications by Citations

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118  
papers

22,374  
citations

49  
h-index

134  
g-index

134  
ext. papers

26,346  
ext. citations

14.6  
avg, IF

6.76  
L-index

#	Paper	IF	Citations
118	Identification and analysis of functional elements in 1% of the human genome by the ENCODE pilot project. <i>Nature</i> , <b>2007</b> , 447, 799-816	50.4	4121
117	Evolutionarily conserved elements in vertebrate, insect, worm, and yeast genomes. <i>Genome Research</i> , <b>2005</b> , 15, 1034-50	9.7	2643
116	Sequence and comparative analysis of the chicken genome provide unique perspectives on vertebrate evolution. <i>Nature</i> , <b>2004</b> , 432, 695-716	50.4	2143
115	Detection of nonneutral substitution rates on mammalian phylogenies. <i>Genome Research</i> , <b>2010</b> , 20, 110-17	3.7	1338
114	Evolutionary and biomedical insights from the rhesus macaque genome. <i>Science</i> , <b>2007</b> , 316, 222-34	33.3	1072
113	A high-resolution map of human evolutionary constraint using 29 mammals. <i>Nature</i> , <b>2011</b> , 478, 476-82	50.4	802
112	An RNA gene expressed during cortical development evolved rapidly in humans. <i>Nature</i> , <b>2006</b> , 443, 167-70	50.4	691
111	Comparative analyses of multi-species sequences from targeted genomic regions. <i>Nature</i> , <b>2003</b> , 424, 788-93	50.4	508
110	Comparative and demographic analysis of orang-utan genomes. <i>Nature</i> , <b>2011</b> , 469, 529-33	50.4	431
109	Patterns of positive selection in six Mammalian genomes. <i>PLoS Genetics</i> , <b>2008</b> , 4, e1000144	6	405
108	Analysis of nascent RNA identifies a unified architecture of initiation regions at mammalian promoters and enhancers. <i>Nature Genetics</i> , <b>2014</b> , 46, 1311-20	36.3	399
107	Identification and classification of conserved RNA secondary structures in the human genome. <i>PLoS Computational Biology</i> , <b>2006</b> , 2, e33	5	394
106	Bayesian inference of ancient human demography from individual genome sequences. <i>Nature Genetics</i> , <b>2011</b> , 43, 1031-4	36.3	387
105	A distal enhancer and an ultraconserved exon are derived from a novel retroposon. <i>Nature</i> , <b>2006</b> , 441, 87-90	50.4	384
104	A rapid, extensive, and transient transcriptional response to estrogen signaling in breast cancer cells. <i>Cell</i> , <b>2011</b> , 145, 622-34	56.2	377
103	Genome sequencing highlights the dynamic early history of dogs. <i>PLoS Genetics</i> , <b>2014</b> , 10, e1004016	6	372
102	A simple genetic architecture underlies morphological variation in dogs. <i>PLoS Biology</i> , <b>2010</b> , 8, e1000451	9.7	331

101	Forces shaping the fastest evolving regions in the human genome. <i>PLoS Genetics</i> , <b>2006</b> , 2, e168	6	306
100	Ancient gene flow from early modern humans into Eastern Neanderthals. <i>Nature</i> , <b>2016</b> , 530, 429-33	50.4	269
99	Widespread regulatory activity of vertebrate microRNA* species. <i>Rna</i> , <b>2011</b> , 17, 312-26	5.8	261
98	Phylogenetic estimation of context-dependent substitution rates by maximum likelihood. <i>Molecular Biology and Evolution</i> , <b>2004</b> , 21, 468-88	8.3	245
97	PHAST and RPHAST: phylogenetic analysis with space/time models. <i>Briefings in Bioinformatics</i> , <b>2011</b> , 12, 41-51	13.4	240
96	Signaling pathways differentially affect RNA polymerase II initiation, pausing, and elongation rate in cells. <i>Molecular Cell</i> , <b>2013</b> , 50, 212-22	17.6	231
95	28-way vertebrate alignment and conservation track in the UCSC Genome Browser. <i>Genome Research</i> , <b>2007</b> , 17, 1797-808	9.7	204
94	Genome-wide inference of ancestral recombination graphs. <i>PLoS Genetics</i> , <b>2014</b> , 10, e1004342	6	200
93	A computer program designed to screen rapidly for HIV type 1 intersubtype recombinant sequences. <i>AIDS Research and Human Retroviruses</i> , <b>1995</b> , 11, 1413-6	1.6	185
92	Fast, scalable prediction of deleterious noncoding variants from functional and population genomic data. <i>Nature Genetics</i> , <b>2017</b> , 49, 618-624	36.3	178
91	A method for calculating probabilities of fitness consequences for point mutations across the human genome. <i>Nature Genetics</i> , <b>2015</b> , 47, 276-83	36.3	175
90	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> , <b>2007</b> , 27, 5090-104	4.8	166
89	Combining phylogenetic and hidden Markov models in biosequence analysis. <i>Journal of Computational Biology</i> , <b>2004</b> , 11, 413-28	1.7	166
88	Analyses of deep mammalian sequence alignments and constraint predictions for 1% of the human genome. <i>Genome Research</i> , <b>2007</b> , 17, 760-74	9.7	163
87	Evolutionary and population genomics of the cavity causing bacteria <i>Streptococcus mutans</i> . <i>Molecular Biology and Evolution</i> , <b>2013</b> , 30, 881-93	8.3	133
86	New Methods for Detecting Lineage-Specific Selection. <i>Lecture Notes in Computer Science</i> , <b>2006</b> , 190-205	5.9	114
85	Identification of active transcriptional regulatory elements from GRO-seq data. <i>Nature Methods</i> , <b>2015</b> , 12, 433-8	21.6	112
84	The completion of the Mammalian Gene Collection (MGC). <i>Genome Research</i> , <b>2009</b> , 19, 2324-33	9.7	98

83	Genome-wide inference of natural selection on human transcription factor binding sites. <i>Nature Genetics</i> , <b>2013</b> , 45, 723-9	36.3	95
82	Three periods of regulatory innovation during vertebrate evolution. <i>Science</i> , <b>2011</b> , 333, 1019-24	33.3	92
81	Sequencing and comparative analysis of a conserved syntenic segment in the Solanaceae. <i>Genetics</i> , <b>2008</b> , 180, 391-408	4	84
80	The draft genome sequence of the ferret ( <i>Mustela putorius furo</i> ) facilitates study of human respiratory disease. <i>Nature Biotechnology</i> , <b>2014</b> , 32, 1250-5	44.5	81
79	GAGA factor maintains nucleosome-free regions and has a role in RNA polymerase II recruitment to promoters. <i>PLoS Genetics</i> , <b>2015</b> , 11, e1005108	6	63
78	Analyses of X-linked and autosomal genetic variation in population-scale whole genome sequencing. <i>Nature Genetics</i> , <b>2011</b> , 43, 741-3	36.3	63
77	Inference of natural selection from interspersed genomic elements based on polymorphism and divergence. <i>Molecular Biology and Evolution</i> , <b>2013</b> , 30, 1159-71	8.3	58
76	Distinguishing noise from signal in patterns of genomic divergence in a highly polymorphic avian radiation. <i>Molecular Ecology</i> , <b>2015</b> , 24, 4238-51	5.7	56
75	Demographically-Based Evaluation of Genomic Regions under Selection in Domestic Dogs. <i>PLoS Genetics</i> , <b>2016</b> , 12, e1005851	6	56
74	Gene regulation by CcpA and catabolite repression explored by RNA-Seq in <i>Streptococcus mutans</i> . <i>PLoS ONE</i> , <b>2013</b> , 8, e60465	3.7	54
73	A model-based analysis of GC-biased gene conversion in the human and chimpanzee genomes. <i>PLoS Genetics</i> , <b>2013</b> , 9, e1003684	6	52
72	The role of GC-biased gene conversion in shaping the fastest evolving regions of the human genome. <i>Molecular Biology and Evolution</i> , <b>2012</b> , 29, 1047-57	8.3	52
71	Diversity of miRNAs, siRNAs, and piRNAs across 25 <i>Drosophila</i> cell lines. <i>Genome Research</i> , <b>2014</b> , 24, 1236-50	9.7	50
70	Computational screening of conserved genomic DNA in search of functional noncoding elements. <i>Nature Methods</i> , <b>2005</b> , 2, 535-45	21.6	50
69	Phylogenetic Hidden Markov Models <b>2005</b> , 325-351		48
68	Is a super-enhancer greater than the sum of its parts?. <i>Nature Genetics</i> , <b>2016</b> , 49, 2-3	36.3	44
67	Accurate prediction of inducible transcription factor binding intensities in vivo. <i>PLoS Genetics</i> , <b>2012</b> , 8, e1002610	6	43
66	Inversion Medians Outperform Breakpoint Medians in Phylogeny Reconstruction from Gene-Order Data. <i>Lecture Notes in Computer Science</i> , <b>2002</b> , 521-536	0.9	42

65	Darwinian alchemy: Human genes from noncoding DNA. <i>Genome Research</i> , <b>2009</b> , 19, 1693-5	9.7	41
64	A simplified hillslope erosion model with vegetation elements for practical applications. <i>Journal of Hydrology</i> , <b>2002</b> , 258, 111-121	6	41
63	Comparative genomic analysis of the <i>Streptococcus dysgalactiae</i> species group: gene content, molecular adaptation, and promoter evolution. <i>Genome Biology and Evolution</i> , <b>2011</b> , 3, 168-85	3.9	40
62	Contrasting X-linked and autosomal diversity across 14 human populations. <i>American Journal of Human Genetics</i> , <b>2014</b> , 94, 827-44	11	39
61	Dynamic evolution of regulatory element ensembles in primate CD4 T cells. <i>Nature Ecology and Evolution</i> , <b>2018</b> , 2, 537-548	12.3	38
60	Targeted discovery of novel human exons by comparative genomics. <i>Genome Research</i> , <b>2007</b> , 17, 1763-73	9.7	38
59	Computational identification of evolutionarily conserved exons <b>2004</b> ,		36
58	Phylogenomics of primates and their ancestral populations. <i>Genome Research</i> , <b>2009</b> , 19, 1929-41	9.7	35
57	A community-maintained standard library of population genetic models. <i>ELife</i> , <b>2020</b> , 9,	8.9	35
56	Positive selection on apoptosis related genes. <i>FEBS Letters</i> , <b>2010</b> , 584, 469-76	3.8	31
55	Finding an Optimal Inversion Median: Experimental Results. <i>Lecture Notes in Computer Science</i> , <b>2001</b> , 189-203	0.9	30
54	The impact of age, biogenesis, and genomic clustering on <i>Drosophila</i> microRNA evolution. <i>Rna</i> , <b>2013</b> , 19, 1295-308	5.8	29
53	Error and error mitigation in low-coverage genome assemblies. <i>PLoS ONE</i> , <b>2011</b> , 6, e17034	3.7	29
52	New genes often acquire male-specific functions but rarely become essential in. <i>Genes and Development</i> , <b>2017</b> , 31, 1841-1846	12.6	28
51	Diverse modes of evolutionary emergence and flux of conserved microRNA clusters. <i>Rna</i> , <b>2014</b> , 20, 1850-63	5.8	27
50	Adaptive evolution of testis-specific, recently evolved, clustered miRNAs in <i>Drosophila</i> . <i>Rna</i> , <b>2014</b> , 20, 1195-209	5.8	27
49	Mapping gene flow between ancient hominins through demography-aware inference of the ancestral recombination graph. <i>PLoS Genetics</i> , <b>2020</b> , 16, e1008895	6	27
48	PhastWeb: a web interface for evolutionary conservation scoring of multiple sequence alignments using phastCons and phyloP. <i>Bioinformatics</i> , <b>2019</b> , 35, 2320-2322	7.2	27

47	An algorithm to enumerate sorting reversals for signed permutations. <i>Journal of Computational Biology</i> , <b>2003</b> , 10, 575-97	1.7	25
46	Scikit-ribo Enables Accurate Estimation and Robust Modeling of Translation Dynamics at Codon Resolution. <i>Cell Systems</i> , <b>2018</b> , 6, 180-191.e4	10.6	24
45	Cis-regulatory elements and human evolution. <i>Current Opinion in Genetics and Development</i> , <b>2014</b> , 29, 81-9	4.9	24
44	Replacing and additive horizontal gene transfer in Streptococcus. <i>Molecular Biology and Evolution</i> , <b>2012</b> , 29, 3309-20	8.3	23
43	Deep experimental profiling of microRNA diversity, deployment, and evolution across the genus. <i>Genome Research</i> , <b>2018</b> , 28, 52-65	9.7	22
42	Efficient approximations for learning phylogenetic HMM models from data. <i>Bioinformatics</i> , <b>2004</b> , 20 Suppl 1, i161-8	7.2	21
41	An integration platform for heterogeneous bioinformatics software components. <i>IBM Systems Journal</i> , <b>2001</b> , 40, 570-591		21
40	The Genome Sequence DataBase: towards an integrated functional genomics resource. <i>Nucleic Acids Research</i> , <b>1999</b> , 27, 35-8	20.1	21
39	Combining phylogenetic and hidden Markov models in biosequence analysis <b>2003</b> ,		21
38	Accelerated sequence divergence of conserved genomic elements in <i>Drosophila melanogaster</i> . <i>Genome Research</i> , <b>2008</b> , 18, 1592-601	9.7	19
37	An algorithm to enumerate all sorting reversals <b>2002</b> ,		19
36	An evolutionary framework for measuring epigenomic information and estimating cell-type-specific fitness consequences. <i>Nature Genetics</i> , <b>2019</b> , 51, 335-342	36.3	16
35	Nascent RNA sequencing reveals a dynamic global transcriptional response at genes and enhancers to the natural medicinal compound celastrol. <i>Genome Research</i> , <b>2017</b> , 27, 1816-1829	9.7	15
34	The Genome Sequence DataBase version 1.0 (GSDB): from low pass sequences to complete genomes. <i>Nucleic Acids Research</i> , <b>1997</b> , 25, 18-23	20.1	15
33	The Genome Sequence DataBase (GSDB): improving data quality and data access. <i>Nucleic Acids Research</i> , <b>1998</b> , 26, 21-6	20.1	15
32	An inferred fitness consequence map of the rice genome. <i>Nature Plants</i> , <b>2020</b> , 6, 119-130	11.5	14
31	Estimation of allele-specific fitness effects across human protein-coding sequences and implications for disease. <i>Genome Research</i> , <b>2019</b> , 29, 1310-1321	9.7	14
30	Challenges in funding and developing genomic software: roots and remedies. <i>Genome Biology</i> , <b>2019</b> , 20, 147	18.3	13

29	Population genomic analysis reveals a rich speciation and demographic history of orang-utans ( <i>Pongo pygmaeus</i> and <i>Pongo abelii</i> ). <i>PLoS ONE</i> , <b>2013</b> , 8, e77175	3.7	12
28	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> , <b>2020</b> , 117, 30554-30563	11.5	9
27	From Summary Statistics to Gene Trees: Methods for Inferring Positive Selection. <i>Trends in Genetics</i> , <b>2020</b> , 36, 243-258	8.5	8
26	Reconstructing histories of complex gene clusters on a phylogeny. <i>Journal of Computational Biology</i> , <b>2010</b> , 17, 1267-79	1.7	8
25	Reconstructing the Evolutionary History of Complex Human Gene Clusters <b>2008</b> , 29-49		8
24	A community-maintained standard library of population genetic models		7
23	Inference of Ancestral Recombination Graphs Using ARGweaver. <i>Methods in Molecular Biology</i> , <b>2020</b> , 2090, 231-266	1.4	6
22	Evolutionary history reconstruction for Mammalian complex gene clusters. <i>Journal of Computational Biology</i> , <b>2009</b> , 16, 1051-70	1.7	5
21	Characterizing RNA stability genome-wide through combined analysis of PRO-seq and RNA-seq data. <i>BMC Biology</i> , <b>2021</b> , 19, 30	7.3	5
20	Extreme purifying selection against point mutations in the human genome		5
19	Phylogenetic Modeling of Regulatory Element Turnover Based on Epigenomic Data. <i>Molecular Biology and Evolution</i> , <b>2020</b> , 37, 2137-2152	8.3	4
18	Characterizing RNA stability genome-wide through combined analysis of PRO-seq and RNA-seq data		4
17	Enabling large-scale next-generation sequence assembly with Blacklight. <i>Concurrency Computation Practice and Experience</i> , <b>2014</b> , 26, 2157-2166	1.4	3
16	Bioinformatics for rice resources. <i>Novartis Foundation Symposium</i> , <b>2001</b> , 236, 59-81; discussion 81-4		2
15	Long-read sequencing reveals rapid evolution of immunity- and cancer-related genes in bats		2
14	Reconstructing Histories of Complex Gene Clusters on a Phylogeny. <i>Lecture Notes in Computer Science</i> , <b>2009</b> , 150-163	0.9	2
13	Probabilities of Fitness Consequences for Point Mutations Across the Human Genome		2
12	Fast, scalable prediction of deleterious noncoding variants from functional and population genomic data		2

11	Estimation of allele-specific fitness effects across human protein-coding sequences and implications for disease	2
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9	Genomic islands of differentiation in a rapid avian radiation have been driven by recent selective sweeps	1
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6	phastWeb: a web interface for evolutionary conservation scoring of multiple sequence alignments using phastCons and phyloP	1
5	Nascent RNA sequencing reveals a dynamic global transcriptional response at genes and enhancers to the natural medicinal compound celastrol	1
4	Circadian immunity, sunrise time and the seasonality of respiratory infections <b>2021</b> ,	1
3	A multiple genome alignment workflow shows the impact of repeat masking and parameter tuning on alignment of functional regions in plants	1
2	ACE: a probabilistic model for characterizing gene-level essentiality in CRISPR screens. <i>Genome Biology</i> , <b>2021</b> , 22, 278	18.3 1
1	A multiple alignment workflow shows the effect of repeat masking and parameter tuning on alignment in plants.. <i>Plant Genome</i> , <b>2022</b> , e20204	4.4 0