## Adam C Siepel

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/4099094/publications.pdf Version: 2024-02-01



#	Article	IF	CITATIONS
1	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
2	Evolutionarily conserved elements in vertebrate, insect, worm, and yeast genomes. Genome Research, 2005, 15, 1034-1050.	5.5	3,517
3	Sequence and comparative analysis of the chicken genome provide unique perspectives on vertebrate evolution. Nature, 2004, 432, 695-716.	27.8	2,421
4	Detection of nonneutral substitution rates on mammalian phylogenies. Genome Research, 2010, 20, 110-121.	5.5	1,878
5	Evolutionary and Biomedical Insights from the Rhesus Macaque Genome. Science, 2007, 316, 222-234.	12.6	1,283
6	A high-resolution map of human evolutionary constraint using 29 mammals. Nature, 2011, 478, 476-482.	27.8	1,016
7	An RNA gene expressed during cortical development evolved rapidly in humans. Nature, 2006, 443, 167-172.	27.8	884
8	Comparative analyses of multi-species sequences from targeted genomic regions. Nature, 2003, 424, 788-793.	27.8	584
9	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
10	Comparative and demographic analysis of orang-utan genomes. Nature, 2011, 469, 529-533.	27.8	541
11	Patterns of Positive Selection in Six Mammalian Genomes. PLoS Genetics, 2008, 4, e1000144.	3.5	529
12	Bayesian inference of ancient human demography from individual genome sequences. Nature Genetics, 2011, 43, 1031-1034.	21.4	526
13	Genome Sequencing Highlights the Dynamic Early History of Dogs. PLoS Genetics, 2014, 10, e1004016.	3.5	481
14	A Rapid, Extensive, and Transient Transcriptional Response to Estrogen Signaling in Breast Cancer Cells. Cell, 2011, 145, 622-634.	28.9	458
15	A distal enhancer and an ultraconserved exon are derived from a novel retroposon. Nature, 2006, 441, 87-90.	27.8	452
16	Identification and Classification of Conserved RNA Secondary Structures in the Human Genome. PLoS Computational Biology, 2006, 2, e33.	3.2	439
17	A Simple Genetic Architecture Underlies Morphological Variation in Dogs. PLoS Biology, 2010, 8, e1000451.	5.6	429
18	Forces Shaping the Fastest Evolving Regions in the Human Genome. PLoS Genetics, 2006, 2, e168.	3.5	399

2

#	Article	IF	CITATIONS
19	PHAST and RPHAST: phylogenetic analysis with space/time models. Briefings in Bioinformatics, 2011, 12, 41-51.	6.5	396
20	Ancient gene flow from early modern humans into Eastern Neanderthals. Nature, 2016, 530, 429-433.	27.8	392
21	Phylogenetic Estimation of Context-Dependent Substitution Rates by Maximum Likelihood. Molecular Biology and Evolution, 2003, 21, 468-488.	8.9	351
22	Genome-Wide Inference of Ancestral Recombination Graphs. PLoS Genetics, 2014, 10, e1004342.	3.5	323
23	Signaling Pathways Differentially Affect RNA Polymerase II Initiation, Pausing, and Elongation Rate in Cells. Molecular Cell, 2013, 50, 212-222.	9.7	300
24	Fast, scalable prediction of deleterious noncoding variants from functional and population genomic data. Nature Genetics, 2017, 49, 618-624.	21.4	299
25	Widespread regulatory activity of vertebrate microRNA* species. Rna, 2011, 17, 312-326.	3.5	293
26	A method for calculating probabilities of fitness consequences for point mutations across the human genome. Nature Genetics, 2015, 47, 276-283.	21.4	247
27	28-Way vertebrate alignment and conservation track in the UCSC Genome Browser. Genome Research, 2007, 17, 1797-1808.	5.5	237
28	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
29	Combining Phylogenetic and Hidden Markov Models in Biosequence Analysis. Journal of Computational Biology, 2004, 11, 413-428.	1.6	207
30	Identification of active transcriptional regulatory elements from GRO-seq data. Nature Methods, 2015, 12, 433-438.	19.0	198
31	Analyses of deep mammalian sequence alignments and constraint predictions for 1% of the human genome. Genome Research, 2007, 17, 760-774.	5.5	184
32	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
33	Evolutionary and Population Genomics of the Cavity Causing Bacteria Streptococcus mutans. Molecular Biology and Evolution, 2013, 30, 881-893.	8.9	168
34	New Methods for Detecting Lineage-Specific Selection. Lecture Notes in Computer Science, 2006, , 190-205.	1.3	158
35	Three Periods of Regulatory Innovation During Vertebrate Evolution. Science, 2011, 333, 1019-1024.	12.6	127
36	The completion of the Mammalian Gene Collection (MGC). Genome Research, 2009, 19, 2324-2333.	5.5	125

#	Article	IF	CITATIONS
37	Genome-wide inference of natural selection on human transcription factor binding sites. Nature Genetics, 2013, 45, 723-729.	21.4	121
38	A community-maintained standard library of population genetic models. ELife, 2020, 9, .	6.0	112
39	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
40	Sequencing and Comparative Analysis of a Conserved Syntenic Segment in the Solanaceae. Genetics, 2008, 180, 391-408.	2.9	105
41	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
42	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
43	Analyses of X-linked and autosomal genetic variation in population-scale whole genome sequencing. Nature Genetics, 2011, 43, 741-743.	21.4	81
44	Phylogenetic Hidden Markov Models. , 2005, , 325-351.		78
45	Inference of Natural Selection from Interspersed Genomic Elements Based on Polymorphism and Divergence. Molecular Biology and Evolution, 2013, 30, 1159-1171.	8.9	77
46	Demographically-Based Evaluation of Genomic Regions under Selection in Domestic Dogs. PLoS Genetics, 2016, 12, e1005851.	3.5	77
47	Mapping gene flow between ancient hominins through demography-aware inference of the ancestral recombination graph. PLoS Genetics, 2020, 16, e1008895.	3.5	76
48	A Model-Based Analysis of GC-Biased Gene Conversion in the Human and Chimpanzee Genomes. PLoS Genetics, 2013, 9, e1003684.	3.5	74
49	Gene Regulation by CcpA and Catabolite Repression Explored by RNA-Seq in Streptococcus mutans. PLoS ONE, 2013, 8, e60465.	2.5	74
50	Distinguishing noise from signal in patterns of genomic divergence in a highly polymorphic avian radiation. Molecular Ecology, 2015, 24, 4238-4251.	3.9	72
51	New genes often acquire male-specific functions but rarely become essential in <i>Drosophila</i> . Genes and Development, 2017, 31, 1841-1846.	5.9	71
52	Is a super-enhancer greater than the sum of its parts?. Nature Genetics, 2017, 49, 2-3.	21.4	70
53	Darwinian alchemy: Human genes from noncoding DNA. Genome Research, 2009, 19, 1693-1695.	5.5	66
54	Diversity of miRNAs, siRNAs, and piRNAs across 25 <i>Drosophila</i> cell lines. Genome Research, 2014, 24, 1236-1250.	5.5	66

#	Article	IF	CITATIONS
55	Dynamic evolution of regulatory element ensembles in primate CD4+ T cells. Nature Ecology and Evolution, 2018, 2, 537-548.	7.8	65
56	Contrasting X-Linked and Autosomal Diversity across 14 Human Populations. American Journal of Human Genetics, 2014, 94, 827-844.	6.2	61
57	Computational identification of evolutionarily conserved exons. , 2004, , .		56
58	Accurate Prediction of Inducible Transcription Factor Binding Intensities In Vivo. PLoS Genetics, 2012, 8, e1002610.	3.5	56
59	Phylogenomics of primates and their ancestral populations. Genome Research, 2009, 19, 1929-1941.	5.5	53
60	Computational screening of conserved genomic DNA in search of functional noncoding elements. Nature Methods, 2005, 2, 535-545.	19.0	52
61	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
62	Cis-regulatory elements and human evolution. Current Opinion in Genetics and Development, 2014, 29, 81-89.	3.3	51
63	Inversion Medians Outperform Breakpoint Medians in Phylogeny Reconstruction from Gene-Order Data. Lecture Notes in Computer Science, 2002, , 521-536.	1.3	51
64	A simplified hillslope erosion model with vegetation elements for practical applications. Journal of Hydrology, 2002, 258, 111-121.	5.4	47
65	Adaptive evolution of testis-specific, recently evolved, clustered miRNAs in <i>Drosophila</i> . Rna, 2014, 20, 1195-1209.	3.5	47
66	PhastWeb: a web interface for evolutionary conservation scoring of multiple sequence alignments using phastCons and phyloP. Bioinformatics, 2019, 35, 2320-2322.	4.1	44
67	Targeted discovery of novel human exons by comparative genomics. Genome Research, 2007, 17, 1763-1773.	5.5	42
68	Scikit-ribo Enables Accurate Estimation and Robust Modeling of Translation Dynamics at Codon Resolution. Cell Systems, 2018, 6, 180-191.e4.	6.2	41
69	Diverse modes of evolutionary emergence and flux of conserved microRNA clusters. Rna, 2014, 20, 1850-1863.	3.5	40
70	Finding an Optimal Inversion Median: Experimental Results. Lecture Notes in Computer Science, 2001, , 189-203.	1.3	40
71	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
72	Deep experimental profiling of microRNA diversity, deployment, and evolution across the <i>Drosophila</i> genus. Genome Research, 2018, 28, 52-65.	5.5	39

#	Article	IF	CITATIONS
73	Positive selection on apoptosis related genes. FEBS Letters, 2010, 584, 469-476.	2.8	38
74	Characterizing RNA stability genome-wide through combined analysis of PRO-seq and RNA-seq data. BMC Biology, 2021, 19, 30.	3.8	38
75	The impact of age, biogenesis, and genomic clustering on <i>Drosophila</i> microRNA evolution. Rna, 2013, 19, 1295-1308.	3.5	35
76	Error and Error Mitigation in Low-Coverage Genome Assemblies. PLoS ONE, 2011, 6, e17034.	2.5	33
77	Replacing and Additive Horizontal Gene Transfer in Streptococcus. Molecular Biology and Evolution, 2012, 29, 3309-3320.	8.9	33
78	An evolutionary framework for measuring epigenomic information and estimating cell-type-specific fitness consequences. Nature Genetics, 2019, 51, 335-342.	21.4	33
79	An integration platform for heterogeneous bioinformatics software components. IBM Systems Journal, 2001, 40, 570-591.	3.0	32
80	An Algorithm to Enumerate Sorting Reversals for Signed Permutations. Journal of Computational Biology, 2003, 10, 575-597.	1.6	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.	5.5	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.	6.7	28
84	Efficient approximations for learning phylogenetic HMM models from data. Bioinformatics, 2004, 20, i161-i168.	4.1	27
85	Inference of Ancestral Recombination Graphs Using ARGweaver. Methods in Molecular Biology, 2020, 2090, 231-266.	0.9	27
86	A Deep-Learning Approach for Inference of Selective Sweeps from the Ancestral Recombination Graph. Molecular Biology and Evolution, 2022, 39, .	8.9	27
87	The Genome Sequence DataBase: towards an integrated functional genomics resource. Nucleic Acids Research, 1999, 27, 35-38.	14.5	26
88	Estimation of allele-specific fitness effects across human protein-coding sequences and implications for disease. Genome Research, 2019, 29, 1310-1321.	5.5	24
89	Accelerated sequence divergence of conserved genomic elements in Drosophila melanogaster. Genome Research, 2008, 18, 1592-1601.	5.5	23
90	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

#	Article	IF	CITATIONS
91	Challenges in funding and developing genomic software: roots and remedies. Genome Biology, 2019, 20, 147.	8.8	21
92	An algorithm to enumerate all sorting reversals. , 2002, , .		20
93	An inferred fitness consequence map of the rice genome. Nature Plants, 2020, 6, 119-130.	9.3	20
94	The Genome Sequence DataBase (GSDB): improving data quality and data access. Nucleic Acids Research, 1998, 26, 21-26.	14.5	19
95	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
96	Phylogenetic Modeling of Regulatory Element Turnover Based on Epigenomic Data. Molecular Biology and Evolution, 2020, 37, 2137-2152.	8.9	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. Journal of Computational Biology, 2010, 17, 1267-1279.	1.6	8
99	Enabling largeâ€scale nextâ€generation sequence assembly with Blacklight. Concurrency Computation Practice and Experience, 2014, 26, 2157-2166.	2.2	8
100	Evolutionary History Reconstruction for Mammalian Complex Gene Clusters. Journal of Computational Biology, 2009, 16, 1051-1070.	1.6	7
101	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
102	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
103	ACE: a probabilistic model for characterizing gene-level essentiality in CRISPR screens. Genome Biology, 2021, 22, 278.	8.8	3
104	Bioinformatics for Rice Resources. Novartis Foundation Symposium, 2001, 236, 59-84.	1.1	2
105	Reconstructing Histories of Complex Gene Clusters on a Phylogeny. Lecture Notes in Computer Science, 2009, , 150-163.	1.3	2