Jeffrey D Jensen

List of Publications by Year
in descending order

120 papers	12,456 citations	47006 47 h-index	31849 101 g-index
141 all docs	141 docs citations	141 times ranked	15573 citing authors

#	Article	IF	Citations
1	A Draft Sequence of the Neandertal Genome. Science, 2010, 328, 710-722.	12.6	3,588
2	Resequencing 50 accessions of cultivated and wild rice yields markers for identifying agronomically important genes. Nature Biotechnology, 2012, 30, 105-111.	17.5	818
3	Complete Resequencing of 40 Genomes Reveals Domestication Events and Genes in Silkworm () Tj ETQq1 1 0.784314 rgBT /Overlock 10	12.6	342
4	Experimental illumination of a fitness landscape. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 7896-7901.	7.1	289
5	Adaptive Evolution of Multiple Traits Through Multiple Mutations at a Single Gene. Science, 2013, 339, 1312-1316.	12.6	277
6	Loci associated with skin pigmentation identified in African populations. Science, 2017, 358, .	12.6	260
7	Adaptive introgression underlies polymorphic seasonal camouflage in snowshoe hares. Science, 2018, 360, 1355-1358.	12.6	234
8	Distinguishing Between Selective Sweeps and Demography Using DNA Polymorphism Data. Genetics, 2005, 170, 1401-1410.	2.9	229
9	On the Origin and Spread of an Adaptive Allele in Deer Mice. Science, 2009, 325, 1095-1098.	12.6	228
10	A Critical Assessment of Storytelling: Gene Ontology Categories and the Importance of Validating Genomic Scans. Molecular Biology and Evolution, 2012, 29, 3237-3248.	8.9	220
11	Population genetic inference from genomic sequence variation. Genome Research, 2010, 20, 291-300.	5.5	200
12	Extensive Genome-Wide Variability of Human Cytomegalovirus in Congenitally Infected Infants. PLoS Pathogens, 2011, 7, e1001344.	4.7	196
13	Controlling the False-Positive Rate in Multilocus Genome Scans for Selection. Genetics, 2007, 175, 737-750.	2.9	163
14	Antiviral drug resistance as an adaptive process. Virus Evolution, 2016, 2, vew014.	4.9	162
15	The consequences of not accounting for background selection in demographic inference. Molecular Ecology, 2016, 25, 135-141.	3.9	160
16	Searching for Footprints of Positive Selection in Whole-Genome SNP Data From Nonequilibrium Populations. Genetics, 2010, 185, 907-922.	2.9	159
17	Rapid Intrahost Evolution of Human Cytomegalovirus Is Shaped by Demography and Positive Selection. PLoS Genetics, 2013, 9, e1003735.	3.5	144
18	Influenza Virus Drug Resistance: A Time-Sampled Population Genetics Perspective. PLoS Genetics, 2014, 10, e1004185.	3.5	126

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19	On the unfounded enthusiasm for soft selective sweeps. Nature Communications, 2014, 5, 5281.	12.8	126
20	<scp>WFABC</scp>: a <scp>W</scp>right–<scp>F</scp>isher <scp>ABC</scp>‐based approach for inferring effective population sizes and selection coefficients from time‐sampled data. Molecular Ecology Resources, 2015, 15, 87-98.	4.8	126
21	Linking a mutation to survival in wild mice. Science, 2019, 363, 499-504.	12.6	126
22	The importance of the Neutral Theory in 1968 and 50 years on: A response to Kern and Hahn 2018. Evolution; International Journal of Organic Evolution, 2019, 73, 111-114.	2.3	123
23	Progress and prospects in mapping recent selection in the genome. Heredity, 2007, 98, 340-348.	2.6	121
24	Thinking too positive? Revisiting current methods of population genetic selection inference. Trends in Genetics, 2014, 30, 540-546.	6.7	121
25	Toward an Evolutionarily Appropriate Null Model: Jointly Inferring Demography and Purifying Selection. Genetics, 2020, 215, 173-192.	2.9	119
26	A Systematic Survey of an Intragenic Epistatic Landscape. Molecular Biology and Evolution, 2015, 32, 229-238.	8.9	118
27	SHIFTING FITNESS LANDSCAPES IN RESPONSE TO ALTERED ENVIRONMENTS. Evolution; International Journal of Organic Evolution, 2013, 67, 3512-3522.	2.3	114
28	Human-Specific Histone Methylation Signatures at Transcription Start Sites in Prefrontal Neurons. PLoS Biology, 2012, 10, e1001427.	5.6	113
29	On the (un)predictability of a large intragenic fitness landscape. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 14085-14090.	7.1	104
30	Genomic Variation and Its Impact on Gene Expression in Drosophila melanogaster. PLoS Genetics, 2012, 8, e1003055.	3.5	102
31	Limits and patterns of cytomegalovirus genomic diversity in humans. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, E4120-E4128.	7.1	101
32	A Bayesian MCMC Approach to Assess the Complete Distribution of Fitness Effects of New Mutations: Uncovering the Potential for Adaptive Walks in Challenging Environments. Genetics, 2014, 196, 841-852.	2.9	100
33	An Approximate Bayesian Estimator Suggests Strong, Recurrent Selective Sweeps in Drosophila. PLoS Genetics, 2008, 4, e1000198.	3.5	94
34	Approaches for identifying targets of positive selection. Trends in Genetics, 2007, 23, 568-577.	6.7	89
35	To Pool, or Not to Pool?. Genetics, 2010, 186, 41-43.	2.9	86
36	On the Utility of Linkage Disequilibrium as a Statistic for Identifying Targets of Positive Selection in Nonequilibrium Populations. Genetics, 2007, 176, 2371-2379.	2.9	84

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37	The past, present and future of genomic scans for selection. Molecular Ecology, 2016, 25, 1-4.	3.9	80
38	On the unfounded enthusiasm for soft selective sweeps II: Examining recent evidence from humans, flies, and viruses. PLoS Genetics, 2018, 14, e1007859.	3.5	79
39	The Evolutionary History of Nebraska Deer Mice: Local Adaptation in the Face of Strong Gene Flow. Molecular Biology and Evolution, 2018, 35, 792-806.	8.9	76
40	Human cytomegalovirus intrahost evolution—a new avenue for understanding and controlling herpesvirus infections. Current Opinion in Virology, 2014, 8, 109-115.	5.4	75
41	Two ancient human genomes reveal Polynesian ancestry among the indigenous Botocudos of Brazil. Current Biology, 2014, 24, R1035-R1037.	3.9	73
42	An Approximate Markov Model for the Wright–Fisher Diffusion and Its Application to Time Series Data. Genetics, 2016, 203, 831-846.	2.9	70
43	Accelerated Adaptive Evolution on a Newly Formed X Chromosome. PLoS Biology, 2009, 7, e1000082.	5.6	66
44	The impact of equilibrium assumptions on tests of selection. Frontiers in Genetics, 2013, 4, 235.	2.3	66
45	Worldwide Population Structure, Long-Term Demography, and Local Adaptation of <i>Helicobacter pylori</i>. Genetics, 2015, 200, 947-963.	2.9	65
46	EVIDENCE OF ADAPTATION FROM ANCESTRAL VARIATION IN YOUNG POPULATIONS OF BEACH MICE. Evolution; International Journal of Organic Evolution, 2012, 66, 3209-3223.	2.3	64
47	The SIB Swiss Institute of Bioinformatics' resources: focus on curated databases. Nucleic Acids Research, 2016, 44, D27-D37.	14.5	64
48	Effects of Selection at Linked Sites on Patterns of Genetic Variability. Annual Review of Ecology, Evolution, and Systematics, 2021, 52, 177-197.	8.3	64
49	RECURRENT AND RECENT SELECTIVE SWEEPS IN THE piRNA PATHWAY. Evolution; International Journal of Organic Evolution, 2013, 67, 1081-1090.	2.3	63
50	Recommendations for improving statistical inference in population genomics. PLoS Biology, 2022, 20, e3001669.	5.6	60
51	The population genomics of rapid adaptation: disentangling signatures of selection and demography in white sands lizards. Molecular Ecology, 2016, 25, 306-323.	3.9	56
52	The Impact of Purifying and Background Selection on the Inference of Population History: Problems and Prospects. Molecular Biology and Evolution, 2021, 38, 2986-3003.	8.9	56
53	Characterizing the Influence of Effective Population Size on the Rate of Adaptation: Gillespie's Darwin Domain. Genome Biology and Evolution, 2011, 3, 687-701.	2.5	52
54	Recent Progress in Polymorphism-Based Population Genetic Inference. Journal of Heredity, 2012, 103, 287-296.	2.4	51

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55	CRISPR-Cas9â€"mediated saturated mutagenesis screen predicts clinical drug resistance with improved accuracy. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, 11751-11756.	7.1	50
56	On the importance of skewed offspring distributions and background selection in virus population genetics. Heredity, 2016, 117, 393-399.	2.6	48
57	Similar Levels of X-linked and Autosomal Nucleotide Variation in African and non-African populations of Drosophila melanogaster. BMC Evolutionary Biology, 2007, 7, 202.	3.2	46
58	Evolution of the Influenza A Virus Genome during Development of Oseltamivir Resistance<i>In Vitro</i>. Journal of Virology, 2014, 88, 272-281.	3.4	45
59	A Statistical Guide to the Design of Deep Mutational Scanning Experiments. Genetics, 2016, 204, 77-87.	2.9	45
60	Coalescent Processes with Skewed Offspring Distributions and Nonequilibrium Demography. Genetics, 2018, 208, 323-338.	2.9	45
61	On the Prospect of Identifying Adaptive Loci in Recently Bottlenecked Populations. PLoS ONE, 2014, 9, e110579.	2.5	44
62	The genomic history of the Aegean palatial civilizations. Cell, 2021, 184, 2565-2586.e21.	28.9	43
63	On the Analysis of Intrahost and Interhost Viral Populations: Human Cytomegalovirus as a Case Study of Pitfalls and Expectations. Journal of Virology, 2017, 91, .	3.4	39
64	On the relative roles of background selection and genetic hitchhiking in shaping human cytomegalovirus genetic diversity. Molecular Ecology, 2016, 25, 403-413.	3.9	37
65	Inferring Demography and Selection in Organisms Characterized by Skewed Offspring Distributions. Genetics, 2019, 211, 1019-1028.	2.9	37
66	Mutations in Influenza A Virus Neuraminidase and Hemagglutinin Confer Resistance against a Broadly Neutralizing Hemagglutinin Stem Antibody. Journal of Virology, 2019, 93, .	3.4	37
67	An experimental evaluation of drugâ€induced mutational meltdown as an antiviral treatment strategy. Evolution; International Journal of Organic Evolution, 2016, 70, 2470-2484.	2.3	36
68	A Balance between Inhibitor Binding and Substrate Processing Confers Influenza Drug Resistance. Journal of Molecular Biology, 2016, 428, 538-553.	4.2	36
69	Experimental adaptation of human echovirus 11 to ultraviolet radiation leads to resistance to disinfection and ribavirin. Virus Evolution, 2017, 3, vex035.	4.9	33
70	Characterizing human cytomegalovirus reinfection in congenitally infected infants: an evolutionary perspective. Molecular Ecology, 2017, 26, 1980-1990.	3.9	31
71	Phylogenetic incongruence in the Drosophila melanogaster species group. Molecular Phylogenetics and Evolution, 2007, 43, 1138-1150.	2.7	30
72	Targeted resequencing of a genomic region influencing tameness and aggression reveals multiple signals of positive selection. Heredity, 2011, 107, 205-214.	2.6	30

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73	Resistance of Echovirus 11 to ClO_2 Is Associated with Enhanced Host Receptor Use, Altered Entry Routes, and High Fitness. Environmental Science & Technology, 2017, 51, 10746-10755.	10.0	29
74	The Origin and Spread of Locally Adaptive Seasonal Camouflage in Snowshoe Hares. American Naturalist, 2020, 196, 316-332.	2.1	29
75	The Combined Effect of Oseltamivir and Favipiravir on Influenza A Virus Evolution. Genome Biology and Evolution, 2017, 9, 1913-1924.	2.5	28
76	On the prospect of achieving accurate joint estimation of selection with population history. Genome Biology and Evolution, 2022, 14, .	2.5	28
77	Detecting and Quantifying Changing Selection Intensities from Time-Sampled Polymorphism Data. G3: Genes, Genomes, Genetics, 2016, 6, 893-904.	1.8	27
78	The Demographic History of African Drosophila melanogaster. Genome Biology and Evolution, 2018, 10, 2338-2342.	2.5	26
79	The population genetics of crypsis in vertebrates: recent insights from mice, hares, and lizards. Heredity, 2020, 124, 1-14.	2.6	24
80	Considering mutational meltdown as a potential SARS-CoV-2 treatment strategy. Heredity, 2020, 124, 619-620.	2.6	24
81	How Can We Resolve Lewontin€™s Paradox?. Genome Biology and Evolution, 2022, 14, .	2.5	24
82	Inferring the age of a fixed beneficial allele. Molecular Ecology, 2016, 25, 157-169.	3.9	23
83	Inferences of Demography and Selection in an African Population of *Drosophila melanogaster*. Genetics, 2013, 193, 215-228.	2.9	21
84	On the Demographic and Selective Forces Shaping Patterns of Human Cytomegalovirus Variation within Hosts. Pathogens, 2018, 7, 16.	2.8	21
85	The fitness landscape of the codon space across environments. Heredity, 2018, 121, 422-437.	2.6	21
86	Molecular Basis for Differential Patterns of Drug Resistance in Influenza N1 and N2 Neuraminidase. Journal of Chemical Theory and Computation, 2016, 12, 6098-6108.	5.3	20
87	Imposed mutational meltdown as an antiviral strategy. Evolution; International Journal of Organic Evolution, 2020, 74, 2549-2559.	2.3	20
88	Common Polymorphisms in the Glycoproteins of Human Cytomegalovirus and Associated Strain-Specific Immunity. Viruses, 2021, 13, 1106.	3.3	20
89	Two sides of the same coin: A population genetics perspective on lethal mutagenesis and mutational meltdown. Virus Evolution, 2017, 3, vex004.	4.9	19
90	Convergent evolution of seasonal camouflage in response to reduced snow cover across the snowshoe hare range*. Evolution; International Journal of Organic Evolution, 2020, 74, 2033-2045.	2.3	19

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91	Patterns of Sequence Variability and Divergence at the diminutive Gene Region of Drosophila melanogaster: Complex Patterns Suggest an Ancestral Selective Sweep. Genetics, 2007, 177, 1071-1085.	2.9	18
92	Characterizing Recurrent Positive Selection at Fast-Evolving Genes in Drosophila miranda and Drosophila pseudoobscura. Genome Biology and Evolution, 2010, 2, 371-378.	2.5	17
93	The Genomic Signature of Population Reconnection Following Isolation: From Theory to HIV. G3: Genes, Genomes, Genetics, 2016, 6, 107-120.	1.8	17
94	Positive Selection Drives Preferred Segment Combinations during Influenza Virus Reassortment. Molecular Biology and Evolution, 2015, 32, 1519-1532.	8.9	16
95	Synonymous Mutations at the Beginning of the Influenza A Virus Hemagglutinin Gene Impact Experimental Fitness. Journal of Molecular Biology, 2018, 430, 1098-1115.	4.2	16
96	On Characterizing Adaptive Events Unique to Modern Humans. Genome Biology and Evolution, 2011, 3, 791-798.	2.5	15
97	Soft selective sweeps: Addressing new definitions, evaluating competing models, and interpreting empirical outliers. PLoS Genetics, 2022, 18, e1010022.	3.5	15
98	Evaluating the contributions of purifying selection and progeny-skew in dictating within-host <i>Mycobacterium tuberculosis</i> evolution. Evolution; International Journal of Organic Evolution, 2020, 74, 992-1001.	2.3	14
99	Revisiting the notion of deleterious sweeps. Genetics, 2021, 219, .	2.9	14
100	Inferring Selection in Partially Sequenced Regions. Molecular Biology and Evolution, 2008, 25, 438-446.	8.9	13
101	Structural Determination of the Broadly Reactive Anti-IGHV1-69 Anti-idiotypic Antibody G6 and Its Idiotope. Cell Reports, 2017, 21, 3243-3255.	6.4	13
102	On Reconciling Single and Recurrent Hitchhiking Models. Genome Biology and Evolution, 2009, 1, 320-324.	2.5	12
103	The evolution of gene expression and binding specificity of the largest transcription factor family in primates. Evolution; International Journal of Organic Evolution, 2016, 70, 167-180.	2.3	12
104	Evidence for a Selective Sweep on Chromosome 1 of Cultivated Sorghum. Crop Science, 2006, 46, S-27.	1.8	11
105	The Impact of Linked Selection in Chimpanzees: A Comparative Study. Genome Biology and Evolution, 2016, 8, 3202-3208.	2.5	11
106	A consideration of within-host human cytomegalovirus genetic variation. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 816-817.	7.1	11
107	Considering Genomic Scans for Selection as Coalescent Model Choice. Genome Biology and Evolution, 2020, 12, 871-877.	2.5	10
108	Evaluating the ability of the pairwise joint site frequency spectrum to co-estimate selection and demography. Frontiers in Genetics, 2015, 6, 268.	2.3	9

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109	The population genomics of within-host Mycobacterium tuberculosis. Heredity, 2021, 126, 1-9.	2.6	8
110	Studying Population Genetic Processes in Viruses: From Drug-Resistance Evolution to Patient Infection Dynamics. , 2021, , 227-232.		7
111	Inferring the Evolutionary History of Primate microRNA Binding Sites: Overcoming Motif Counting Biases. Molecular Biology and Evolution, 2014, 31, 1894-1901.	8.9	6
112	PopPlanner: visually constructing demographic models for simulation. Frontiers in Genetics, 2015, 6, 150.	2.3	6
113	Inferring the distribution of fitness effects in patient-sampled and experimental virus populations: two case studies. Heredity, 2022, 128, 79-87.	2.6	4
114	Recent evidence for pervasive adaptation targeting gene expression attributable to population size change. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, E109-10; author reply 111.	7.1	3
115	On Detecting Selective Sweeps Using Single Genomes. Frontiers in Genetics, 2011, 2, 85.	2.3	3
116	Distinguishing neutral from deleterious mutations in growing populations. Frontiers in Genetics, 2014, 5, 7.	2.3	3
117	The impact of frequently neglected model violations on bacterial recombination rate estimation: a case study in <i>Mycobacterium canettii</i> and <i>Mycobacterium tuberculosis</i>. G3: Genes, Genomes, Genetics, 2022, , .	1.8	3
118	Some complexities in interpreting apparent effects of hitchhiking: A commentary on Gompert et al.Â(2022). Molecular Ecology, 0, , .	3.9	3
119	Quantifying polymorphism and divergence from epigenetic data: a framework for inferring the action of selection. Frontiers in Genetics, 2015, 6, 190.	2.3	0
120	Identification of a permissive secondary mutation that restores the enzymatic activity of oseltamivir resistance mutation H275Y. Journal of Virology, 2022, , jvi0198221.	3.4	0