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	Identification of a permissive secondary mutation that restores the enzymatic activity of oseltamivir resistance mutation H275Y. Journal of Virology, 2022, , jvi0198221.	3.4	0
2	Inferring the distribution of fitness effects in patient-sampled and experimental virus populations: two case studies. Heredity, 2022, 128, 79-87.	2.6	4
3	Soft selective sweeps: Addressing new definitions, evaluating competing models, and interpreting empirical outliers. PLoS Genetics, 2022, 18, e1010022.	3.5	15
4	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
5	Recommendations for improving statistical inference in population genomics. PLoS Biology, 2022, 20, e3001669.	5.6	60
6	How Can We Resolve Lewontin's Paradox?. Genome Biology and Evolution, 2022, 14, .	2.5	24
7	On the prospect of achieving accurate joint estimation of selection with population history. Genome Biology and Evolution, 2022, 14, .	2.5	28
8	The population genomics of within-host Mycobacterium tuberculosis. Heredity, 2021, 126, 1-9.	2.6	8
9	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
10	The genomic history of the Aegean palatial civilizations. Cell, 2021, 184, 2565-2586.e21.	28.9	43
11	Revisiting the notion of deleterious sweeps. Genetics, 2021, 219, .	2.9	14
12	Common Polymorphisms in the Glycoproteins of Human Cytomegalovirus and Associated Strain-Specific Immunity. Viruses, 2021, 13, 1106.	3.3	20
13	Studying Population Genetic Processes in Viruses: From Drug-Resistance Evolution to Patient Infection Dynamics. , 2021, , 227-232.		7
14	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
15	The population genetics of crypsis in vertebrates: recent insights from mice, hares, and lizards. Heredity, 2020, 124, 1-14.	2.6	24
16	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
17	Imposed mutational meltdown as an antiviral strategy. Evolution; International Journal of Organic Evolution, 2020, 74, 2549-2559.	2.3	20
18	Considering Genomic Scans for Selection as Coalescent Model Choice. Genome Biology and Evolution, 2020, 12, 871-877.	2.5	10

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19	The Origin and Spread of Locally Adaptive Seasonal Camouflage in Snowshoe Hares. American Naturalist, 2020, 196, 316-332.	2.1	29
20	Toward an Evolutionarily Appropriate Null Model: Jointly Inferring Demography and Purifying Selection. Genetics, 2020, 215, 173-192.	2.9	119
21	Considering mutational meltdown as a potential SARS-CoV-2 treatment strategy. Heredity, 2020, 124, 619-620.	2.6	24
22	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
23	Evaluating the contributions of purifying selection and progeny‐skew in dictating within‐host *Mycobacterium tuberculosis* evolution. Evolution; International Journal of Organic Evolution, 2020, 74, 992-1001.	2.3	14
24	Linking a mutation to survival in wild mice. Science, 2019, 363, 499-504.	12.6	126
25	Inferring Demography and Selection in Organisms Characterized by Skewed Offspring Distributions. Genetics, 2019, 211, 1019-1028.	2.9	37
26	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
27	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
28	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
29	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
30	Coalescent Processes with Skewed Offspring Distributions and Nonequilibrium Demography. Genetics, 2018, 208, 323-338.	2.9	45
31	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
32	The Demographic History of African Drosophila melanogaster. Genome Biology and Evolution, 2018, 10, 2338-2342.	2.5	26
33	On the Demographic and Selective Forces Shaping Patterns of Human Cytomegalovirus Variation within Hosts. Pathogens, 2018, 7, 16.	2.8	21
34	The fitness landscape of the codon space across environments. Heredity, 2018, 121, 422-437.	2.6	21
35	Adaptive introgression underlies polymorphic seasonal camouflage in snowshoe hares. Science, 2018, 360, 1355-1358.	12.6	234
36	Characterizing human cytomegalovirus reinfection in congenitally infected infants: an evolutionary perspective. Molecular Ecology, 2017, 26, 1980-1990.	3.9	31

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37	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
38	Loci associated with skin pigmentation identified in African populations. Science, 2017, 358, .	12.6	260
39	CRISPR-Cas9–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
40	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
41	The Combined Effect of Oseltamivir and Favipiravir on Influenza A Virus Evolution. Genome Biology and Evolution, 2017, 9, 1913-1924.	2.5	28
42	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
43	Two sides of the same coin: A population genetics perspective on lethal mutagenesis and mutational meltdown. Virus Evolution, 2017, 3, vex004.	4.9	19
44	Experimental adaptation of human echovirus 11 to ultraviolet radiation leads to resistance to disinfection and ribavirin. Virus Evolution, 2017, 3, vex035.	4.9	33
45	The Impact of Linked Selection in Chimpanzees: A Comparative Study. Genome Biology and Evolution, 2016, 8, 3202-3208.	2.5	11
46	Inferring the age of a fixed beneficial allele. Molecular Ecology, 2016, 25, 157-169.	3.9	23
47	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
48	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
49	The consequences of not accounting for background selection in demographic inference. Molecular Ecology, 2016, 25, 135-141.	3.9	160
50	An Approximate Markov Model for the Wright–Fisher Diffusion and Its Application to Time Series Data. Genetics, 2016, 203, 831-846.	2.9	70
51	An experimental evaluation of drug–induced mutational meltdown as an antiviral treatment strategy. Evolution; International Journal of Organic Evolution, 2016, 70, 2470-2484.	2.3	36
52	A Statistical Guide to the Design of Deep Mutational Scanning Experiments. Genetics, 2016, 204, 77-87.	2.9	45
53	On the importance of skewed offspring distributions and background selection in virus population genetics. Heredity, 2016, 117, 393-399.	2.6	48
54	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

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55	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
56	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
57	Antiviral drug resistance as an adaptive process. Virus Evolution, 2016, 2, vew014.	4.9	162
58	Detecting and Quantifying Changing Selection Intensities from Time-Sampled Polymorphism Data. G3: Genes, Genomes, Genetics, 2016, 6, 893-904.	1.8	27
59	The Genomic Signature of Population Reconnection Following Isolation: From Theory to HIV. G3: Genes, Genomes, Genetics, 2016, 6, 107-120.	1.8	17
60	A Balance between Inhibitor Binding and Substrate Processing Confers Influenza Drug Resistance. Journal of Molecular Biology, 2016, 428, 538-553.	4.2	36
61	The past, present and future of genomic scans for selection. Molecular Ecology, 2016, 25, 1-4.	3.9	80
62	The SIB Swiss Institute of Bioinformatics' resources: focus on curated databases. Nucleic Acids Research, 2016, 44, D27-D37.	14.5	64
63	WFABC: a Wright–Fisher ABC–based approach for inferring effective population sizes and selection coefficients from time-sampled data. Molecular Ecology Resources, 2015, 15, 87-98.	4.8	126
64	PopPlanner: visually constructing demographic models for simulation. Frontiers in Genetics, 2015, 6, 150.	2.3	6
65	Quantifying polymorphism and divergence from epigenetic data: a framework for inferring the action of selection. Frontiers in Genetics, 2015, 6, 190.	2.3	0
66	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
67	Positive Selection Drives Preferred Segment Combinations during Influenza Virus Reassortment. Molecular Biology and Evolution, 2015, 32, 1519-1532.	8.9	16
68	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
69	Worldwide Population Structure, Long-Term Demography, and Local Adaptation of *Helicobacter pylori*. Genetics, 2015, 200, 947-963.	2.9	65
70	A Systematic Survey of an Intragenic Epistatic Landscape. Molecular Biology and Evolution, 2015, 32, 229-238.	8.9	118
71	Distinguishing neutral from deleterious mutations in growing populations. Frontiers in Genetics, 2014, 5, 7.	2.3	3
72	Influenza Virus Drug Resistance: A Time-Sampled Population Genetics Perspective. PLoS Genetics, 2014, 10, e1004185.	3.5	126

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73	Thinking too positive? Revisiting current methods of population genetic selection inference. Trends in Genetics, 2014, 30, 540-546.	6.7	121
74	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
75	Evolution of the Influenza A Virus Genome during Development of Oseltamivir Resistance *In Vitro*. Journal of Virology, 2014, 88, 272-281.	3.4	45
76	Two ancient human genomes reveal Polynesian ancestry among the indigenous Botocudos of Brazil. Current Biology, 2014, 24, R1035-R1037.	3.9	73
77	On the unfounded enthusiasm for soft selective sweeps. Nature Communications, 2014, 5, 5281.	12.8	126
78	Human cytomegalovirus intrahost evolution—a new avenue for understanding and controlling herpesvirus infections. Current Opinion in Virology, 2014, 8, 109-115.	5.4	75
79	Inferring the Evolutionary History of Primate microRNA Binding Sites: Overcoming Motif Counting Biases. Molecular Biology and Evolution, 2014, 31, 1894-1901.	8.9	6
80	On the Prospect of Identifying Adaptive Loci in Recently Bottlenecked Populations. PLoS ONE, 2014, 9, e110579.	2.5	44
81	Adaptive Evolution of Multiple Traits Through Multiple Mutations at a Single Gene. Science, 2013, 339, 1312-1316.	12.6	277
82	SHIFTING FITNESS LANDSCAPES IN RESPONSE TO ALTERED ENVIRONMENTS. Evolution; International Journal of Organic Evolution, 2013, 67, 3512-3522.	2.3	114
83	Rapid Intrahost Evolution of Human Cytomegalovirus Is Shaped by Demography and Positive Selection. PLoS Genetics, 2013, 9, e1003735.	3.5	144
84	Inferences of Demography and Selection in an African Population of *Drosophila melanogaster*. Genetics, 2013, 193, 215-228.	2.9	21
85	RECURRENT AND RECENT SELECTIVE SWEEPS IN THE piRNA PATHWAY. Evolution; International Journal of Organic Evolution, 2013, 67, 1081-1090.	2.3	63
86	The impact of equilibrium assumptions on tests of selection. Frontiers in Genetics, 2013, 4, 235.	2.3	66
87	Genomic Variation and Its Impact on Gene Expression in Drosophila melanogaster. PLoS Genetics, 2012, 8, e1003055.	3.5	102
88	Recent Progress in Polymorphism-Based Population Genetic Inference. Journal of Heredity, 2012, 103, 287-296.	2.4	51
89	Resequencing 50 accessions of cultivated and wild rice yields markers for identifying agronomically important genes. Nature Biotechnology, 2012, 30, 105-111.	17.5	818
90	Human-Specific Histone Methylation Signatures at Transcription Start Sites in Prefrontal Neurons. PLoS Biology, 2012, 10, e1001427.	5.6	113

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91	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
92	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
93	On Detecting Selective Sweeps Using Single Genomes. Frontiers in Genetics, 2011, 2, 85.	2.3	3
94	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
95	Targeted resequencing of a genomic region influencing tameness and aggression reveals multiple signals of positive selection. Heredity, 2011, 107, 205-214.	2.6	30
96	On Characterizing Adaptive Events Unique to Modern Humans. Genome Biology and Evolution, 2011, 3, 791-798.	2.5	15
97	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
98	Extensive Genome-Wide Variability of Human Cytomegalovirus in Congenitally Infected Infants. PLoS Pathogens, 2011, 7, e1001344.	4.7	196
99	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
100	A Draft Sequence of the Neandertal Genome. Science, 2010, 328, 710-722.	12.6	3,588
101	To Pool, or Not to Pool?. Genetics, 2010, 186, 41-43.	2.9	86
102	Searching for Footprints of Positive Selection in Whole-Genome SNP Data From Nonequilibrium Populations. Genetics, 2010, 185, 907-922.	2.9	159
103	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
104	Population genetic inference from genomic sequence variation. Genome Research, 2010, 20, 291-300.	5.5	200
105	Complete Resequencing of 40 Genomes Reveals Domestication Events and Genes in Silkworm () Tj ETQq1 1 0.784314 rgBT /Overlock	12.6	342
106	Accelerated Adaptive Evolution on a Newly Formed X Chromosome. PLoS Biology, 2009, 7, e1000082.	5.6	66
107	On Reconciling Single and Recurrent Hitchhiking Models. Genome Biology and Evolution, 2009, 1, 320-324.	2.5	12
108	On the Origin and Spread of an Adaptive Allele in Deer Mice. Science, 2009, 325, 1095-1098.	12.6	228

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109	Inferring Selection in Partially Sequenced Regions. Molecular Biology and Evolution, 2008, 25, 438-446.	8.9	13
110	An Approximate Bayesian Estimator Suggests Strong, Recurrent Selective Sweeps in Drosophila. PLoS Genetics, 2008, 4, e1000198.	3.5	94
111	Controlling the False-Positive Rate in Multilocus Genome Scans for Selection. Genetics, 2007, 175, 737-750.	2.9	163
112	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
113	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
114	Phylogenetic incongruence in the Drosophila melanogaster species group. Molecular Phylogenetics and Evolution, 2007, 43, 1138-1150.	2.7	30
115	Progress and prospects in mapping recent selection in the genome. Heredity, 2007, 98, 340-348.	2.6	121
116	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
117	Approaches for identifying targets of positive selection. Trends in Genetics, 2007, 23, 568-577.	6.7	89
118	Evidence for a Selective Sweep on Chromosome 1 of Cultivated Sorghum. Crop Science, 2006, 46, S-27.	1.8	11
119	Distinguishing Between Selective Sweeps and Demography Using DNA Polymorphism Data. Genetics, 2005, 170, 1401-1410.	2.9	229
120	Some complexities in interpreting apparent effects of hitchhiking: A commentary on Gompert et al.Â(2022). Molecular Ecology, 0, , .	3.9	3