

# Yuseob Kim

## List of Publications by Year in descending order

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Version: 2024-02-01

43  
papers

3,813  
citations

279798

23  
h-index

254184

43  
g-index

48  
all docs

48  
docs citations

48  
times ranked

4087  
citing authors

#	ARTICLE	IF	CITATIONS
1	Genomic scans for selective sweeps using SNP data. <i>Genome Research</i> , 2005, 15, 1566-1575.	5.5	891
2	Detecting a Local Signature of Genetic Hitchhiking Along a Recombining Chromosome. <i>Genetics</i> , 2002, 160, 765-777.	2.9	567
3	Linkage Disequilibrium as a Signature of Selective Sweeps. <i>Genetics</i> , 2004, 167, 1513-1524.	2.9	382
4	Pattern of polymorphism after strong artificial selection in a domestication event. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004, 101, 10667-10672.	7.1	295
5	Distinguishing Between Selective Sweeps and Demography Using DNA Polymorphism Data. <i>Genetics</i> , 2005, 170, 1401-1410.	2.9	229
6	Joint Effects of Genetic Hitchhiking and Background Selection on Neutral Variation. <i>Genetics</i> , 2000, 155, 1415-1427.	2.9	179
7	Spread of an Inactive Form of Caspase-12 in Humans Is Due to Recent Positive Selection. <i>American Journal of Human Genetics</i> , 2006, 78, 659-670.	6.2	149
8	Selective Sweeps in the Presence of Interference Among Partially Linked Loci. <i>Genetics</i> , 2003, 164, 389-398.	2.9	86
9	Adaptation in Sexuals vs. Asexuals: Clonal Interference and the Fisher-Muller Model. <i>Genetics</i> , 2005, 171, 1377-1386.	2.9	85
10	A Pseudohitchhiking Model of X vs. Autosomal Diversity. <i>Genetics</i> , 2004, 168, 2261-2269.	2.9	81
11	An Adaptive Hypothesis for the Evolution of the Y Chromosome. <i>Genetics</i> , 1998, 150, 1693-1698.	2.9	73
12	Detecting Local Adaptation Using the Joint Sampling of Polymorphism Data in the Parental and Derived Populations. <i>Genetics</i> , 2008, 179, 1713-1720.	2.9	67
13	A genome-wide scan for signatures of directional selection in domesticated pigs. <i>BMC Genomics</i> , 2015, 16, 130.	2.8	67
14	Allele Frequency Distribution Under Recurrent Selective Sweeps. <i>Genetics</i> , 2006, 172, 1967-1978.	2.9	65
15	Hitchhiking Effect of a Beneficial Mutation Spreading in a Subdivided Population. <i>Genetics</i> , 2011, 189, 213-226.	2.9	52
16	The dynamics of mutations associated with anti-malarial drug resistance in <i>Plasmodium falciparum</i> . <i>Trends in Parasitology</i> , 2009, 25, 557-563.	3.3	42
17	A Composite-Likelihood Method for Detecting Incomplete Selective Sweep from Population Genomic Data. <i>Genetics</i> , 2015, 200, 633-649.	2.9	42
18	Human genomic disease variants: A neutral evolutionary explanation. <i>Genome Research</i> , 2012, 22, 1383-1394.	5.5	41

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19	Identification of a Locus Under Complex Positive Selection in <i>Drosophila simulans</i> by Haplotype Mapping and Composite-Likelihood Estimation. <i>Genetics</i> , 2004, 168, 265-279.	2.9	39
20	Phylogenetic analysis of two <i>Plectus</i> mitochondrial genomes (Nematoda: Plectida) supports a sister group relationship between Plectida and Rhabditida within Chromadorea. <i>Molecular Phylogenetics and Evolution</i> , 2017, 107, 90-102.	2.7	39
21	Effect of Strong Directional Selection on Weakly Selected Mutations at Linked Sites: Implication for Synonymous Codon Usage. <i>Molecular Biology and Evolution</i> , 2003, 21, 286-294.	8.9	34
22	RATE OF ADAPTIVE PEAK SHIFTS WITH PARTIAL GENETIC ROBUSTNESS. <i>Evolution; International Journal of Organic Evolution</i> , 2007, 61, 1847-1856.	2.3	30
23	Purifying Selection Modulates the Estimates of Population Differentiation and Confounds Genome-Wide Comparisons across Single-Nucleotide Polymorphisms. <i>Molecular Biology and Evolution</i> , 2012, 29, 3617-3623.	8.9	28
24	Cetaceans evolution: insights from the genome sequences of common minke whales. <i>BMC Genomics</i> , 2015, 16, 13.	2.8	28
25	Phenotypic Plasticity Promotes Balanced Polymorphism in Periodic Environments by a Genomic Storage Effect. <i>Genetics</i> , 2016, 202, 1437-1448.	2.9	26
26	An analytical model for genetic hitchhiking in the evolution of antimalarial drug resistance. <i>Theoretical Population Biology</i> , 2010, 78, 93-108.	1.1	25
27	Emergence of long-term balanced polymorphism under cyclic selection of spatially variable magnitude. <i>Evolution; International Journal of Organic Evolution</i> , 2015, 69, 979-992.	2.3	25
28	Multiple Modes of Positive Selection Shaping the Patterns of Incomplete Selective Sweeps over African Populations of <i>Drosophila melanogaster</i> . <i>Molecular Biology and Evolution</i> , 2017, 34, 2792-2807.	8.9	21
29	Simulation of DNA sequence evolution under models of recent directional selection. <i>Briefings in Bioinformatics</i> , 2008, 10, 84-96.	6.5	20
30	A Population Genetic Model for the Initial Spread of Partially Resistant Malaria Parasites under Anti-Malarial Combination Therapy and Weak Intra-host Competition. <i>PLoS ONE</i> , 2014, 9, e101601.	2.5	16
31	Signatures of Recent Directional Selection Under Different Models of Population Expansion During Colonization of New Selective Environments. <i>Genetics</i> , 2010, 184, 571-585.	2.9	14
32	Allele frequency changes in artificial selection experiments: statistical power and precision of QTL mapping. <i>Genetical Research</i> , 1999, 73, 177-184.	0.9	12
33	Approximations for the hitchhiking effect caused by the evolution of antimalarial-drug resistance. <i>Journal of Mathematical Biology</i> , 2011, 62, 789-832.	1.9	10
34	Population genetic processes affecting the mode of selective sweeps and effective population size in influenza virus H3N2. <i>BMC Evolutionary Biology</i> , 2016, 16, 156.	3.2	10
35	Urban heat island effect on cicada densities in metropolitan Seoul. <i>PeerJ</i> , 2018, 6, e4238.	2.0	10
36	Partial protection from cyclical selection generates a high level of polymorphism at multiple non-neutral sites. <i>Evolution; International Journal of Organic Evolution</i> , 2019, 73, 1564-1577.	2.3	9

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37	Stochastic patterns of polymorphism after a selective sweep over a subdivided population. <i>Genetical Research</i> , 2013, 95, 57-67.	0.9	5
38	Genetic Hitchhiking under Heterogeneous Spatial Selection Pressures. <i>PLoS ONE</i> , 2013, 8, e61742.	2.5	5
39	The Enrichment of TATA Box and the Scarcity of Depleted Proximal Nucleosome in the Promoters of Duplicated Yeast Genes. <i>Journal of Molecular Evolution</i> , 2010, 70, 69-73.	1.8	4
40	Effects of host and pathogenicity on mutation rates in avian influenza A viruses. <i>Virus Evolution</i> , 2022, 8, veac013.	4.9	4
41	Episodic Nucleotide Substitutions in Seasonal Influenza Virus H3N2 Can Be Explained by Stochastic Genealogical Process without Positive Selection. <i>Molecular Biology and Evolution</i> , 2015, 32, 704-710.	8.9	3
42	Inference of population genetic parameters from an irregular time series of seasonal influenza virus sequences. <i>Genetics</i> , 2021, 217, .	2.9	1
43	Prevalence of negative frequency-dependent selection, revealed by incomplete selective sweeps in African populations of <i>Drosophila melanogaster</i> . <i>BMB Reports</i> , 2018, 51, 1-2.	2.4	1