

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 | Effects of host and pathogenicity on mutation rates in avian influenza A viruses. <i>Virus Evolution</i> , 2022, 8, veac013. | 4.9 | 4 |
| 2 | Inference of population genetic parameters from an irregular time series of seasonal influenza virus sequences. <i>Genetics</i> , 2021, 217, . | 2.9 | 1 |
| 3 | 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 |
| 4 | Urban heat island effect on cicada densities in metropolitan Seoul. <i>PeerJ</i> , 2018, 6, e4238. | 2.0 | 10 |
| 5 | 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 |
| 6 | 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 |
| 7 | 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 |
| 8 | 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 |
| 9 | Phenotypic Plasticity Promotes Balanced Polymorphism in Periodic Environments by a Genomic Storage Effect. <i>Genetics</i> , 2016, 202, 1437-1448. | 2.9 | 26 |
| 10 | 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 |
| 11 | A Composite-Likelihood Method for Detecting Incomplete Selective Sweep from Population Genomic Data. <i>Genetics</i> , 2015, 200, 633-649. | 2.9 | 42 |
| 12 | Cetaceans evolution: insights from the genome sequences of common minke whales. <i>BMC Genomics</i> , 2015, 16, 13. | 2.8 | 28 |
| 13 | A genome-wide scan for signatures of directional selection in domesticated pigs. <i>BMC Genomics</i> , 2015, 16, 130. | 2.8 | 67 |
| 14 | 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 |
| 15 | 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 |
| 16 | Stochastic patterns of polymorphism after a selective sweep over a subdivided population. <i>Genetical Research</i> , 2013, 95, 57-67. | 0.9 | 5 |
| 17 | Genetic Hitchhiking under Heterogeneous Spatial Selection Pressures. <i>PLoS ONE</i> , 2013, 8, e61742. | 2.5 | 5 |
| 18 | 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 |

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|----|--|-----|-----------|
| 19 | Human genomic disease variants: A neutral evolutionary explanation. <i>Genome Research</i> , 2012, 22, 1383-1394. | 5.5 | 41 |
| 20 | 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 |
| 21 | Hitchhiking Effect of a Beneficial Mutation Spreading in a Subdivided Population. <i>Genetics</i> , 2011, 189, 213-226. | 2.9 | 52 |
| 22 | 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 |
| 23 | 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 |
| 24 | 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 |
| 25 | 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 |
| 26 | Simulation of DNA sequence evolution under models of recent directional selection. <i>Briefings in Bioinformatics</i> , 2008, 10, 84-96. | 6.5 | 20 |
| 27 | 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 |
| 28 | RATE OF ADAPTIVE PEAK SHIFTS WITH PARTIAL GENETIC ROBUSTNESS. <i>Evolution; International Journal of Organic Evolution</i> , 2007, 61, 1847-1856. | 2.3 | 30 |
| 29 | 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 |
| 30 | Allele Frequency Distribution Under Recurrent Selective Sweeps. <i>Genetics</i> , 2006, 172, 1967-1978. | 2.9 | 65 |
| 31 | Adaptation in Sexuals vs. Asexuals: Clonal Interference and the Fisher-Muller Model. <i>Genetics</i> , 2005, 171, 1377-1386. | 2.9 | 85 |
| 32 | Genomic scans for selective sweeps using SNP data. <i>Genome Research</i> , 2005, 15, 1566-1575. | 5.5 | 891 |
| 33 | Distinguishing Between Selective Sweeps and Demography Using DNA Polymorphism Data. <i>Genetics</i> , 2005, 170, 1401-1410. | 2.9 | 229 |
| 34 | Linkage Disequilibrium as a Signature of Selective Sweeps. <i>Genetics</i> , 2004, 167, 1513-1524. | 2.9 | 382 |
| 35 | 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 |
| 36 | A Pseudohitchhiking Model of X vs. Autosomal Diversity. <i>Genetics</i> , 2004, 168, 2261-2269. | 2.9 | 81 |

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|----|--|-----|-----------|
| 37 | Pattern of polymorphism after strong artificial selection in a domestication event. Proceedings of the National Academy of Sciences of the United States of America, 2004, 101, 10667-10672. | 7.1 | 295 |
| 38 | Effect of Strong Directional Selection on Weakly Selected Mutations at Linked Sites: Implication for Synonymous Codon Usage. Molecular Biology and Evolution, 2003, 21, 286-294. | 8.9 | 34 |
| 39 | Selective Sweeps in the Presence of Interference Among Partially Linked Loci. Genetics, 2003, 164, 389-398. | 2.9 | 86 |
| 40 | Detecting a Local Signature of Genetic Hitchhiking Along a Recombining Chromosome. Genetics, 2002, 160, 765-777. | 2.9 | 567 |
| 41 | Joint Effects of Genetic Hitchhiking and Background Selection on Neutral Variation. Genetics, 2000, 155, 1415-1427. | 2.9 | 179 |
| 42 | Allele frequency changes in artificial selection experiments: statistical power and precision of QTL mapping. Genetical Research, 1999, 73, 177-184. | 0.9 | 12 |
| 43 | An Adaptive Hypothesis for the Evolution of the Y Chromosome. Genetics, 1998, 150, 1693-1698. | 2.9 | 73 |