Pavlos Pavlidis

List of Publications by Year
in descending order

40 papers	4,069 citations	361413 20 h-index	330143 37 g-index
43 all docs	43 docs citations	43 times ranked	7196 citing authors

#	Article	IF	Citations
1	Significance of regional population HLA immunogenetic datasets in the efficacy of umbilical cord blood banks and marrow donor registries: a study of Cretan HLA genetic diversity. Cytotherapy, 2022, 24, 183-192.	0.7	4
2	Population Genomics Insights into the First Wave of COVID-19. Life, 2021, 11, 129.	2.4	14
3	quickLD: An efficient software for linkage disequilibrium analyses. Molecular Ecology Resources, 2021, 21, 2580-2587.	4.8	7
4	Evolutionary models of amino acid substitutions based on the tertiary structure of their neighborhoods. Proteins: Structure, Function and Bioinformatics, 2021, 89, 1565-1576.	2.6	0
5	Transcriptome reprogramming and myeloid skewing in haematopoietic stem and progenitor cells in systemic lupus erythematosus. Annals of the Rheumatic Diseases, 2020, 79, 242-253.	0.9	44
6	Of dogs and men. Science, 2020, 370, 522-523.	12.6	4
7	Intraspecific diversification of the crop wild relative Brassica cretica Lam. using demographic model selection. BMC Genomics, 2020, 21, 48.	2.8	11
8	Detecting Positive Selection in Populations Using Genetic Data. Methods in Molecular Biology, 2020, 2090, 87-123.	0.9	20
9	qLD: High-performance Computation of Linkage Disequilibrium on CPU and GPU. , 2020, , .		1
10	Comparisons of molecular diversity indices, selective sweeps and population structure of African rice with its wild progenitor and Asian rice. Theoretical and Applied Genetics, 2019, 132, 1145-1158.	3.6	16
11	Independent amylase gene copy number bursts correlate with dietary preferences in mammals. ELife, 2019, 8, .	6.0	78
12	RAiSD detects positive selection based on multiple signatures of a selective sweep and SNP vectors. Communications Biology, 2018, 1, 79.	4.4	97
13	Archaic Hominin Introgression in Africa Contributes to Functional Salivary MUC7 Genetic Variation. Molecular Biology and Evolution, 2017, 34, 2704-2715.	8.9	57
14	A survey of methods and tools to detect recent and strong positive selection. Journal of Biological Research, 2017, 24, 7.	2.1	100
15	VCFtoTree: a user-friendly tool to construct locus-specific alignments and phylogenies from thousands of anthropologically relevant genome sequences. BMC Bioinformatics, 2017, 18, 426.	2.6	14
16	Deploying FPGAs to future-proof genome-wide analyses based on linkage disequilibrium. , 2017, , .		2
17	Recent evolution of the salivary mucin MUC7. Scientific Reports, 2016, 6, 31791.	3.3	30
18	Scalable linkage-disequilibrium-based selective sweep detection: a performance guide. GigaScience, 2016, 5, 7.	6.4	18

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19	The Evolution and Functional Impact of Human Deletion Variants Shared with Archaic Hominin Genomes. Molecular Biology and Evolution, 2015, 32, 1008-1019.	8.9	45
20	1000 Genomes Selection Browser 1.0: a genome browser dedicated to signatures of natural selection in modern humans. Nucleic Acids Research, 2014, 42, D903-D909.	14.5	143
21	Geographic Distribution and Adaptive Significance of Genomic Structural Variants: An Anthropological Genetics Perspective. Human Biology, 2014, 86, 260.	0.2	11
22	Accelerating String Matching on MIC Architecture for Motif Extraction. Lecture Notes in Computer Science, 2014, , 258-267.	1.3	4
23	A general species delimitation method with applications to phylogenetic placements. Bioinformatics, 2013, 29, 2869-2876.	4.1	2,059
24	Primate genome architecture influences structural variation mechanisms and functional consequences. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 15764-15769.	7.1	80
25	CHROMATOGATE: A TOOL FOR DETECTING BASE MIS-CALLS IN MULTIPLE SEQUENCE ALIGNMENTS BY SEMI-AUTOMATIC CHROMATOGRAM INSPECTION. Computational and Structural Biotechnology Journal, 2013, 6, e201303001.	4.1	9
26	SweeD: Likelihood-Based Detection of Selective Sweeps in Thousands of Genomes. Molecular Biology and Evolution, 2013, 30, 2224-2234.	8.9	395
27	Selective Sweep in the Flotillin-2 Region of European Drosophila melanogaster. PLoS ONE, 2013, 8, e56629.	2.5	4
28	Selective Sweep of a cis-Regulatory Sequence in a Non-African Population of Drosophila melanogaster. Molecular Biology and Evolution, 2012, 29, 1167-1174.	8.9	25
29	Selective Sweeps in Multilocus Models of Quantitative Traits. Genetics, 2012, 192, 225-239.	2.9	48
30	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
31	The turbulent life of Sirevirus retrotransposons and the evolution of the maize genome: more than ten thousand elements tell the story. Plant Journal, 2012, 69, 475-488.	5.7	36
32	Exploiting Multi-grain Parallelism for Efficient Selective Sweep Detection. Lecture Notes in Computer Science, 2012, , 56-68.	1.3	6
33	Identification of X-linked quantitative trait loci affecting cold tolerance in Drosophila melanogaster and fine mapping by selective sweep analysis. Molecular Ecology, 2011, 20, 530-544.	3.9	40
34	Inference of seed bank parameters in two wild tomato species using ecological and genetic data. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 17052-17057.	7.1	64
35	Evolution of self-compatibility in Arabidopsis by a mutation in the male specificity gene. Nature, 2010, 464, 1342-1346.	27.8	131
36	Searching for Footprints of Positive Selection in Whole-Genome SNP Data From Nonequilibrium Populations. Genetics, 2010, 185, 907-922.	2.9	159

#	Article	IF	Citations
37	Recent Strong Positive Selection on Drosophila melanogaster HDAC6, a Gene Encoding a Stress Surveillance Factor, as Revealed by Population Genomic Analysis. Molecular Biology and Evolution, 2009, 26, 1549-1556.	8.9	17
38	Meta-coexpression conservation analysis of microarray data: a "subset" approach provides insight into brain-derived neurotrophic factor regulation. BMC Genomics, 2009, 10, 420.	2.8	15
39	Selection on cis-Regulatory Variation at B4galnt2 and Its Influence on von Willebrand Factor in House Mice. Molecular Biology and Evolution, 2008, 26, 567-578.	8.9	23
40	Individualized markers optimize class prediction of microarray data. BMC Bioinformatics, 2006, 7, 345.	2.6	5