

Pavlos Pavlidis

List of Publications by Year in descending order

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Version: 2024-02-01

40
papers

4,069
citations

361296

20
h-index

330025

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. <i>Cytotherapy</i> , 2022, 24, 183-192.	0.3	4
2	Population Genomics Insights into the First Wave of COVID-19. <i>Life</i> , 2021, 11, 129.	1.1	14
3	quickLD: An efficient software for linkage disequilibrium analyses. <i>Molecular Ecology Resources</i> , 2021, 21, 2580-2587.	2.2	7
4	Evolutionary models of amino acid substitutions based on the tertiary structure of their neighborhoods. <i>Proteins: Structure, Function and Bioinformatics</i> , 2021, 89, 1565-1576.	1.5	0
5	Transcriptome reprogramming and myeloid skewing in haematopoietic stem and progenitor cells in systemic lupus erythematosus. <i>Annals of the Rheumatic Diseases</i> , 2020, 79, 242-253.	0.5	44
6	Of dogs and men. <i>Science</i> , 2020, 370, 522-523.	6.0	4
7	Intraspecific diversification of the crop wild relative <i>Brassica cretica</i> Lam. using demographic model selection. <i>BMC Genomics</i> , 2020, 21, 48.	1.2	11
8	Detecting Positive Selection in Populations Using Genetic Data. <i>Methods in Molecular Biology</i> , 2020, 2090, 87-123.	0.4	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. <i>Theoretical and Applied Genetics</i> , 2019, 132, 1145-1158.	1.8	16
11	Independent amylase gene copy number bursts correlate with dietary preferences in mammals. <i>ELife</i> , 2019, 8, .	2.8	78
12	RAiSD detects positive selection based on multiple signatures of a selective sweep and SNP vectors. <i>Communications Biology</i> , 2018, 1, 79.	2.0	97
13	Archaic Hominin Introgression in Africa Contributes to Functional Salivary MUC7 Genetic Variation. <i>Molecular Biology and Evolution</i> , 2017, 34, 2704-2715.	3.5	57
14	A survey of methods and tools to detect recent and strong positive selection. <i>Journal of Biological Research</i> , 2017, 24, 7.	2.2	100
15	VCFtoTree: a user-friendly tool to construct locus-specific alignments and phylogenies from thousands of anthropologically relevant genome sequences. <i>BMC Bioinformatics</i> , 2017, 18, 426.	1.2	14
16	Deploying FPGAs to future-proof genome-wide analyses based on linkage disequilibrium. , 2017, , .		2
17	Recent evolution of the salivary mucin MUC7. <i>Scientific Reports</i> , 2016, 6, 31791.	1.6	30
18	Scalable linkage-disequilibrium-based selective sweep detection: a performance guide. <i>GigaScience</i> , 2016, 5, 7.	3.3	18

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19	The Evolution and Functional Impact of Human Deletion Variants Shared with Archaic Hominin Genomes. <i>Molecular Biology and Evolution</i> , 2015, 32, 1008-1019.	3.5	45
20	1000 Genomes Selection Browser 1.0: a genome browser dedicated to signatures of natural selection in modern humans. <i>Nucleic Acids Research</i> , 2014, 42, D903-D909.	6.5	143
21	Geographic Distribution and Adaptive Significance of Genomic Structural Variants: An Anthropological Genetics Perspective. <i>Human Biology</i> , 2014, 86, 260.	0.4	11
22	Accelerating String Matching on MIC Architecture for Motif Extraction. <i>Lecture Notes in Computer Science</i> , 2014, , 258-267.	1.0	4
23	A general species delimitation method with applications to phylogenetic placements. <i>Bioinformatics</i> , 2013, 29, 2869-2876.	1.8	2,059
24	Primate genome architecture influences structural variation mechanisms and functional consequences. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 15764-15769.	3.3	80
25	CHROMATOGATE: A TOOL FOR DETECTING BASE MIS-CALLS IN MULTIPLE SEQUENCE ALIGNMENTS BY SEMI-AUTOMATIC CHROMATOGRAM INSPECTION. <i>Computational and Structural Biotechnology Journal</i> , 2013, 6, e201303001.	1.9	9
26	SweeD: Likelihood-Based Detection of Selective Sweeps in Thousands of Genomes. <i>Molecular Biology and Evolution</i> , 2013, 30, 2224-2234.	3.5	395
27	Selective Sweep in the Flotillin-2 Region of European <i>Drosophila melanogaster</i> . <i>PLoS ONE</i> , 2013, 8, e56629.	1.1	4
28	Selective Sweep of a cis-Regulatory Sequence in a Non-African Population of <i>Drosophila melanogaster</i> . <i>Molecular Biology and Evolution</i> , 2012, 29, 1167-1174.	3.5	25
29	Selective Sweeps in Multilocus Models of Quantitative Traits. <i>Genetics</i> , 2012, 192, 225-239.	1.2	48
30	A Critical Assessment of Storytelling: Gene Ontology Categories and the Importance of Validating Genomic Scans. <i>Molecular Biology and Evolution</i> , 2012, 29, 3237-3248.	3.5	220
31	The turbulent life of Sirevirus retrotransposons and the evolution of the maize genome: more than ten thousand elements tell the story. <i>Plant Journal</i> , 2012, 69, 475-488.	2.8	36
32	Exploiting Multi-grain Parallelism for Efficient Selective Sweep Detection. <i>Lecture Notes in Computer Science</i> , 2012, , 56-68.	1.0	6
33	Identification of X-linked quantitative trait loci affecting cold tolerance in <i>Drosophila melanogaster</i> and fine mapping by selective sweep analysis. <i>Molecular Ecology</i> , 2011, 20, 530-544.	2.0	40
34	Inference of seed bank parameters in two wild tomato species using ecological and genetic data. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 17052-17057.	3.3	64
35	Evolution of self-compatibility in <i>Arabidopsis</i> by a mutation in the male specificity gene. <i>Nature</i> , 2010, 464, 1342-1346.	13.7	131
36	Searching for Footprints of Positive Selection in Whole-Genome SNP Data From Nonequilibrium Populations. <i>Genetics</i> , 2010, 185, 907-922.	1.2	159

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37	Recent Strong Positive Selection on <i>Drosophila melanogaster</i> HDAC6, a Gene Encoding a Stress Surveillance Factor, as Revealed by Population Genomic Analysis. <i>Molecular Biology and Evolution</i> , 2009, 26, 1549-1556.	3.5	17
38	Meta-coexpression conservation analysis of microarray data: a "subset" approach provides insight into brain-derived neurotrophic factor regulation. <i>BMC Genomics</i> , 2009, 10, 420.	1.2	15
39	Selection on cis-Regulatory Variation at <i>B4galnt2</i> and Its Influence on von Willebrand Factor in House Mice. <i>Molecular Biology and Evolution</i> , 2008, 26, 567-578.	3.5	23
40	Individualized markers optimize class prediction of microarray data. <i>BMC Bioinformatics</i> , 2006, 7, 345.	1.2	5