Panagiotis Ioannidis

List of Publications by Year in descending order

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35 papers 14,141 citations

304743 22 h-index 330143 37 g-index

52 all docs 52 docs citations

times ranked

52

21959 citing authors

#	Article	IF	CITATIONS
1	BUSCO: assessing genome assembly and annotation completeness with single-copy orthologs. Bioinformatics, 2015, 31, 3210-3212.	4.1	9,712
2	BUSCO Applications from Quality Assessments to Gene Prediction and Phylogenomics. Molecular Biology and Evolution, 2018, 35, 543-548.	8.9	1,844
3	OrthoDB v9.1: cataloging evolutionary and functional annotations for animal, fungal, plant, archaeal, bacterial and viral orthologs. Nucleic Acids Research, 2017, 45, D744-D749.	14.5	413
4	OrthoDB v8: update of the hierarchical catalog of orthologs and the underlying free software. Nucleic Acids Research, 2015, 43, D250-D256.	14.5	303
5	Genome of the Asian longhorned beetle (Anoplophora glabripennis), a globally significant invasive species, reveals key functional and evolutionary innovations at the beetle–plant interface. Genome Biology, 2016, 17, 227.	8.8	244
6	Unique features of a global human ectoparasite identified through sequencing of the bed bug genome. Nature Communications, 2016, 7, 10165.	12.8	184
7	A Massive Expansion of Effector Genes Underlies Gall-Formation in the Wheat Pest Mayetiola destructor. Current Biology, 2015, 25, 613-620.	3.9	171
8	Gene content evolution in the arthropods. Genome Biology, 2020, 21, 15.	8.8	150
9	Molecular evolutionary trends and feeding ecology diversification in the Hemiptera, anchored by the milkweed bug genome. Genome Biology, 2019, 20, 64.	8.8	114
10	Genome Sequencing of the Phytoseiid Predatory Mite <i>Metaseiulus occidentalis</i> Reveals Completely Atomized <i>Hox</i> Genes and Superdynamic Intron Evolution. Genome Biology and Evolution, 2016, 8, 1762-1775.	2.5	102
11	Extensive genomic diversity of closely related Wolbachia strains. Microbiology (United Kingdom), 2009, 155, 2211-2222.	1.8	87
12	The Diversity and Evolution of Wolbachia Ankyrin Repeat Domain Genes. PLoS ONE, 2013, 8, e55390.	2.5	80
13	Lucilia cuprina genome unlocks parasitic fly biology to underpin future interventions. Nature Communications, 2015, 6, 7344.	12.8	67
14	Rapid transcriptome sequencing of an invasive pest, the brown marmorated stink bug Halyomorpha halys. BMC Genomics, 2014, 15, 738.	2.8	62
15	Brown marmorated stink bug, Halyomorpha halys (StåI), genome: putative underpinnings of polyphagy, insecticide resistance potential and biology of a top worldwide pest. BMC Genomics, 2020, 21, 227.	2.8	60
16	Genome-enabled insights into the biology of thrips as crop pests. BMC Biology, 2020, 18, 142.	3.8	54
17	Genomic features of the damselfly <i>Calopteryx splendens</i> representing a sister clade to most insect orders. Genome Biology and Evolution, 2017, 9, evx006.	2.5	53
18	Extensively duplicated and transcriptionally active recent lateral gene transfer from a bacterial Wolbachia endosymbiont to its host filarial nematode Brugia malayi. BMC Genomics, 2013, 14, 639.	2.8	37

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19	Developmental plasticity shapes social traits and selection in a facultatively eusocial bee. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 13615-13625.	7.1	37
20	Gene Age Predicts the Strength of Purifying Selection Acting on Gene Expression Variation in Humans. American Journal of Human Genetics, 2014, 95, 660-674.	6.2	35
21	New criteria for selecting the origin of DNA replication in Wolbachia and closely related bacteria. BMC Genomics, 2007, 8, 182.	2.8	34
22	<i>Wolbachia</i> symbiosis and insect immune response. Insect Science, 2008, 15, 89-100.	3.0	31
23	Genomic signatures accompanying the dietary shift to phytophagy in polyphagan beetles. Genome Biology, 2019, 20, 98.	8.8	27
24	Identification and characterization of striking multipleâ€insecticide resistance in a <i>Tetranychus urticae</i> field population from Greece. Pest Management Science, 2021, 77, 666-676.	3.4	23
25	Draft Genome Assembly and Population Genetics of an Agricultural Pollinator, the Solitary Alkali Bee (Halictidae: <i>Nomia melanderi</i>). G3: Genes, Genomes, Genetics, 2019, 9, 625-634.	1.8	19
26	The genome of the stable fly, Stomoxys calcitrans, reveals potential mechanisms underlying reproduction, host interactions, and novel targets for pest control. BMC Biology, 2021, 19, 41.	3.8	19
27	Functionally characterized arthropod pest and pollinator cytochrome P450s associated with xenobiotic metabolism. Pesticide Biochemistry and Physiology, 2022, 181, 105005.	3.6	18
28	Sawfly Genomes Reveal Evolutionary Acquisitions That Fostered the Mega-Radiation of Parasitoid and Eusocial Hymenoptera. Genome Biology and Evolution, 2020, 12, 1099-1188.	2.5	17
29	Efficient genome editing in the olive fruit fly, <scp><i>Bactrocera oleae</i></scp> . Insect Molecular Biology, 2020, 29, 363-372.	2.0	13
30	The Identification and Evolutionary Trends of the Solute Carrier Superfamily in Arthropods. Genome Biology and Evolution, 2020, 12, 1429-1439.	2.5	12
31	Transcriptomic analysis of resistance and short-term induction response to pyrethroids, in Anopheles coluzzii legs. BMC Genomics, 2021, 22, 891.	2.8	11
32	A spatiotemporal atlas of the lepidopteran pest Helicoverpa armigera midgut provides insights into nutrient processing and pH regulation. BMC Genomics, 2022, 23, 75.	2.8	8
33	A transcriptomic and proteomic atlas of expression in the Nezara viridula (Heteroptera: Pentatomidae) midgut suggests the compartmentalization of xenobiotic metabolism and nutrient digestion. BMC Genomics, 2020, 21, 129.	2.8	7
34	Investigating mechanisms associated with emamectin benzoate resistance in the tomato borer Tuta absoluta. Journal of Pest Science, 2022, 95, 1163-1177.	3.7	7
35	Transcriptomic analysis of s-methoprene resistance in the lesser grain borer, Rhyzopertha dominica, and evaluation of piperonyl butoxide as a resistance breaker. BMC Genomics, 2021, 22, 65.	2.8	3