

Alexie Papanicolaou

List of Publications by Year in descending order

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Version: 2024-02-01

47
papers

11,302
citations

236925

25
h-index

214800

47
g-index

50
all docs

50
docs citations

50
times ranked

17863
citing authors

#	ARTICLE	IF	CITATIONS
1	De novo transcript sequence reconstruction from RNA-seq using the Trinity platform for reference generation and analysis. <i>Nature Protocols</i> , 2013, 8, 1494-1512.	12.0	7,054
2	Butterfly genome reveals promiscuous exchange of mimicry adaptations among species. <i>Nature</i> , 2012, 487, 94-98.	27.8	1,086
3	RNA interference in Lepidoptera: An overview of successful and unsuccessful studies and implications for experimental design. <i>Journal of Insect Physiology</i> , 2011, 57, 231-245.	2.0	729
4	The i5K Initiative: Advancing Arthropod Genomics for Knowledge, Human Health, Agriculture, and the Environment. <i>Journal of Heredity</i> , 2013, 104, 595-600.	2.4	358
5	Genomic innovations, transcriptional plasticity and gene loss underlying the evolution and divergence of two highly polyphagous and invasive <i>Helicoverpa</i> pest species. <i>BMC Biology</i> , 2017, 15, 63.	3.8	238
6	Complex modular architecture around a simple toolkit of wing pattern genes. <i>Nature Ecology and Evolution</i> , 2017, 1, 52.	7.8	179
7	Multifaceted biological insights from a draft genome sequence of the tobacco hornworm moth, <i>Manduca sexta</i> . <i>Insect Biochemistry and Molecular Biology</i> , 2016, 76, 118-147.	2.7	154
8	The whole genome sequence of the Mediterranean fruit fly, <i>Ceratitis capitata</i> (Wiedemann), reveals insights into the biology and adaptive evolution of a highly invasive pest species. <i>Genome Biology</i> , 2016, 17, 192.	8.8	130
9	Synteny and Chromosome Evolution in the Lepidoptera: Evidence From Mapping in <i>Heliconius melpomene</i> . <i>Genetics</i> , 2007, 177, 417-426.	2.9	101
10	<i>Heliconius</i> wing patterns: an evo-devo model for understanding phenotypic diversity. <i>Heredity</i> , 2006, 97, 157-167.	2.6	100
11	ButterflyBase: a platform for lepidopteran genomics. <i>Nucleic Acids Research</i> , 2007, 36, D582-D587.	14.5	90
12	Expansion of a bitter taste receptor family in a polyphagous insect herbivore. <i>Scientific Reports</i> , 2016, 6, 23666.	3.3	89
13	Identification and characterization of three chemosensory receptor families in the cotton bollworm <i>Helicoverpa armigera</i> . <i>BMC Genomics</i> , 2014, 15, 597.	2.8	86
14	Characterization of a hotspot for mimicry: assembly of a butterfly wing transcriptome to genomic sequence at the <i>HmYb/Sb</i> locus. <i>Molecular Ecology</i> , 2010, 19, 240-254.	3.9	70
15	Blue: correcting sequencing errors using consensus and context. <i>Bioinformatics</i> , 2014, 30, 2723-2732.	4.1	68
16	Genomewide transcriptional signatures of migratory flight activity in a globally invasive insect pest. <i>Molecular Ecology</i> , 2015, 24, 4901-4911.	3.9	65
17	A phylogenomics approach to characterizing sensory neuron membrane proteins (SNMPs) in Lepidoptera. <i>Insect Biochemistry and Molecular Biology</i> , 2020, 118, 103313.	2.7	63
18	Butterfly genomics eclosing. <i>Heredity</i> , 2008, 100, 150-157.	2.6	60

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19	Chemosensory receptor genes in the Oriental tobacco budworm <i>Helicoverpa assulta</i> . <i>Insect Molecular Biology</i> , 2015, 24, 253-263.	2.0	60
20	Chemosensory genes identified in the antennal transcriptome of the blowfly <i>Calliphora stygia</i> . <i>BMC Genomics</i> , 2015, 16, 255.	2.8	58
21	Transcriptome analysis reveals novel patterning and pigmentation genes underlying <i>Heliconius</i> butterfly wing pattern variation. <i>BMC Genomics</i> , 2012, 13, 288.	2.8	56
22	Next generation transcriptomes for next generation genomes using <i>est2assembly</i> . <i>BMC Bioinformatics</i> , 2009, 10, 447.	2.6	54
23	Transcriptome Analysis of the Sydney Rock Oyster, <i>Saccostrea glomerata</i> : Insights into Molluscan Immunity. <i>PLoS ONE</i> , 2016, 11, e0156649.	2.5	42
24	Comparative genomics of the mimicry switch in <i>Papilio dardanus</i> . <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2014, 281, 20140465.	2.6	40
25	Genomic tools and cDNA derived markers for butterflies. <i>Molecular Ecology</i> , 2005, 14, 2883-2897.	3.9	37
26	Contemporary evolution of a Lepidopteran species, <i>Heliopsis virescens</i> , in response to modern agricultural practices. <i>Molecular Ecology</i> , 2018, 27, 167-181.	3.9	28
27	The draft genome of <i>Actinia tenebrosa</i> reveals insights into toxin evolution. <i>Ecology and Evolution</i> , 2019, 9, 11314-11328.	1.9	28
28	The GMOD Drupal Bioinformatic Server Framework. <i>Bioinformatics</i> , 2010, 26, 3119-3124.	4.1	23
29	Draft Genome of Australian Environmental Strain WM 09.24 of the Opportunistic Human Pathogen <i>Scedosporium aurantiacum</i> . <i>Genome Announcements</i> , 2015, 3, .	0.8	21
30	De novo assembly of the olive fruit fly (<i>Bactrocera oleae</i>) genome with linked-reads and long-read technologies minimizes gaps and provides exceptional Y chromosome assembly. <i>BMC Genomics</i> , 2020, 21, 259.	2.8	21
31	Prior exposure of <i>Arabidopsis</i> seedlings to mechanical stress heightens jasmonic acid-mediated defense against necrotrophic pathogens. <i>BMC Plant Biology</i> , 2020, 20, 548.	3.6	18
32	Characterization of sensory neuron membrane proteins (SNMPs) in cotton bollworm <i>Helicoverpa armigera</i> (Lepidoptera: Noctuidae). <i>Insect Science</i> , 2021, 28, 769-779.	3.0	16
33	OfftargetFinder: a web tool for species-specific RNAi design. <i>Bioinformatics</i> , 2016, 32, 1232-1234.	4.1	14
34	Investigating the NAD-ME biochemical pathway within C4 grasses using transcript and amino acid variation in C4 photosynthetic genes. <i>Photosynthesis Research</i> , 2018, 138, 233-248.	2.9	13
35	Separating two tightly linked species-defining phenotypes in <i>Bactrocera</i> with hybrid recombinant analysis. <i>BMC Genetics</i> , 2020, 21, 132.	2.7	8
36	A Roadmap for Whitefly Genomics Research: Lessons from Previous Insect Genome Projects. <i>Journal of Integrative Agriculture</i> , 2012, 11, 269-280.	3.5	7

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37	The transcriptomic responses of C 4 grasses to subambient CO 2 and low light are largely species specific and only refined by photosynthetic subtype. <i>Plant Journal</i> , 2020, 101, 1170-1184.	5.7	5
38	Disruption of duplicated yellow genes in <i>Bactrocera tryoni</i> modifies pigmentation colouration and impacts behaviour. <i>Journal of Pest Science</i> , 2021, 94, 917-932.	3.7	5
39	The life cycle of a genome project: perspectives and guidelines inspired by insect genome projects. <i>F1000Research</i> , 2016, 5, 18.	1.6	5
40	Novel aquatic silk genes from <i>Simulium (Psilozia) vittatum</i> (Zett) Diptera: Simuliidae. <i>Insect Biochemistry and Molecular Biology</i> , 2013, 43, 1181-1188.	2.7	4
41	The Use of Whole Genome and Next-Generation Sequencing in the Diagnosis of Invasive Fungal Disease. <i>Current Fungal Infection Reports</i> , 2019, 13, 284-291.	2.6	4
42	Identification of interleukin genes in <i>Pogona vitticeps</i> using a de novo transcriptome assembly from RNA-seq data. <i>Immunogenetics</i> , 2016, 68, 719-731.	2.4	3
43	Identification of Putative Nuclear Receptors and Steroidogenic Enzymes in Murray-Darling Rainbowfish (<i>Melanotaenia fluviatilis</i>) Using RNA-Seq and De Novo Transcriptome Assembly. <i>PLoS ONE</i> , 2015, 10, e0142636.	2.5	2
44	Draft Genome Sequence of the Fungus <i>Lecanicillium psalliotae</i> Strain HWLR35, Isolated from a Wheat Leaf Infected with Leaf Rust (Caused by <i>Puccinia triticina</i>). <i>Genome Announcements</i> , 2018, 6, .	0.8	2
45	Molecular Response of the Mediterranean Fruit Fly (Diptera: Tephritidae) to Heat. <i>Journal of Economic Entomology</i> , 2020, 113, 2495-2504.	1.8	2
46	Assessing Differences between Clinical Isolates of <i>Aspergillus fumigatus</i> from Cases of Proven Invasive Aspergillosis and Colonizing Isolates with Respect to Phenotype (Virulence in <i>Tenebrio</i>) <i>Tj ETQq0 0 0 rgBT 4 Overlock 10 Tf 50 37</i>		
47	Mediterranean fruit fly genes exhibit different expression patterns between heat and cold treatments. <i>Bulletin of Entomological Research</i> , 2021, , 1-7.	1.0	0