

# Alexie Papanicolaou

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/4136472/publications.pdf>

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	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> ) Tj ETQq1 1 0.78431.4rgBT /Overlock 10		
2	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
3	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
4	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
5	The transcriptomic responses of C4 grasses to subambient CO2 and low light are largely species specific and only refined by photosynthetic subtype. <i>Plant Journal</i> , 2020, 101, 1170-1184.	5.7	5
6	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
7	Molecular Response of the Mediterranean Fruit Fly (Diptera: Tephritidae) to Heat. <i>Journal of Economic Entomology</i> , 2020, 113, 2495-2504.	1.8	2
8	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
9	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
10	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
11	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
12	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
13	Contemporary evolution of a Lepidopteran species, <i>Heliiothis virescens</i> , in response to modern agricultural practices. <i>Molecular Ecology</i> , 2018, 27, 167-181.	3.9	28
14	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
15	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
16	Complex modular architecture around a simple toolkit of wing pattern genes. <i>Nature Ecology and Evolution</i> , 2017, 1, 52.	7.8	179
17	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
18	Expansion of a bitter taste receptor family in a polyphagous insect herbivore. <i>Scientific Reports</i> , 2016, 6, 23666.	3.3	89

#	ARTICLE	IF	CITATIONS
19	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
20	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
21	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
22	OfftargetFinder: a web tool for species-specific RNAi design. <i>Bioinformatics</i> , 2016, 32, 1232-1234.	4.1	14
23	The life cycle of a genome project: perspectives and guidelines inspired by insect genome projects. <i>F1000Research</i> , 2016, 5, 18.	1.6	5
24	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
25	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
26	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
27	Genomewide transcriptional signatures of migratory flight activity in a globally invasive insect pest. <i>Molecular Ecology</i> , 2015, 24, 4901-4911.	3.9	65
28	Chemosensory receptor genes in the Oriental tobacco budworm <i>Helicoverpa assulta</i> . <i>Insect Molecular Biology</i> , 2015, 24, 253-263.	2.0	60
29	Chemosensory genes identified in the antennal transcriptome of the blowfly <i>Calliphora stygia</i> . <i>BMC Genomics</i> , 2015, 16, 255.	2.8	58
30	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
31	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
32	Blue: correcting sequencing errors using consensus and context. <i>Bioinformatics</i> , 2014, 30, 2723-2732.	4.1	68
33	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
34	Novel aquatic silk genes from <i>Simulium</i> ( <i>Psilozia</i> ) <i>vittatum</i> (Zett) Diptera: Simuliidae. <i>Insect Biochemistry and Molecular Biology</i> , 2013, 43, 1181-1188.	2.7	4
35	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
36	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

#	ARTICLE	IF	CITATIONS
37	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
38	Butterfly genome reveals promiscuous exchange of mimicry adaptations among species. <i>Nature</i> , 2012, 487, 94-98.	27.8	1,086
39	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
40	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
41	The GMOD Drupal Bioinformatic Server Framework. <i>Bioinformatics</i> , 2010, 26, 3119-3124.	4.1	23
42	Next generation transcriptomes for next generation genomes using est2assembly. <i>BMC Bioinformatics</i> , 2009, 10, 447.	2.6	54
43	Butterfly genomics eclosing. <i>Heredity</i> , 2008, 100, 150-157.	2.6	60
44	ButterflyBase: a platform for lepidopteran genomics. <i>Nucleic Acids Research</i> , 2007, 36, D582-D587.	14.5	90
45	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
46	Heliconius wing patterns: an evo-devo model for understanding phenotypic diversity. <i>Heredity</i> , 2006, 97, 157-167.	2.6	100
47	Genomic tools and cDNA derived markers for butterflies. <i>Molecular Ecology</i> , 2005, 14, 2883-2897.	3.9	37