## **Aaron Chuah**

## List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/8649030/publications.pdf

Version: 2024-02-01

30	784	17 h-index	27
papers	citations		g-index
36	36	36	2035
all docs	docs citations	times ranked	citing authors

#	Article	IF	CITATIONS
1	APOE*E2 allele delays age of onset in PSEN1 E280A Alzheimer's disease. Molecular Psychiatry, 2016, 21, 916-924.	7.9	89
2	Functional rare and low frequency variants in BLK and BANK1 contribute to human lupus. Nature Communications, 2019, 10, 2201.	12.8	73
3	The PHF21B gene is associated with major depression and modulates the stress response. Molecular Psychiatry, 2017, 22, 1015-1025.	7.9	56
4	Small RNA changes en route to distinct cellular states of induced pluripotency. Nature Communications, 2014, 5, 5522.	12.8	54
5	T-dependent B cell responses to Plasmodium induce antibodies that form a high-avidity multivalent complex with the circumsporozoite protein. PLoS Pathogens, 2017, 13, e1006469.	4.7	49
6	Genome-wide SNPs reveal fine-scale differentiation among wingless alpine stonefly populations and introgression between winged and wingless forms. Evolution; International Journal of Organic Evolution, 2016, 70, 38-47.	2.3	48
7	Dichloroacetate Prevents Cisplatin-Induced Nephrotoxicity without Compromising Cisplatin Anticancer Properties. Journal of the American Society of Nephrology: JASN, 2016, 27, 3331-3344.	6.1	47
8	Evolution of Vertebrate Phototransduction: Cascade Activation. Molecular Biology and Evolution, 2016, 33, 2064-2087.	8.9	44
9	Tissue and cell-specific transcriptomes in cotton reveal the subtleties of gene regulation underlying the diversity of plant secondary cell walls. BMC Genomics, 2017, 18, 539.	2.8	38
10	Novel and rare functional genomic variants in multiple autoimmune syndrome and Sjögren's syndrome. Journal of Translational Medicine, 2015, 13, 173.	4.4	30
11	Population and phylogenomic decomposition via genotypingâ€byâ€sequencing in Australian <i>Pelargonium</i> . Molecular Ecology, 2016, 25, 2000-2014.	3.9	25
12	The importance of replicating genomic analyses to verify phylogenetic signal for recently evolved lineages. Molecular Ecology, 2016, 25, 3683-3695.	3.9	24
13	Isolation by distance and isolation by environment contribute to population differentiation in Protea repens (Proteaceae L.), a widespread South African species. American Journal of Botany, 2017, 104, 674-684.	1.7	21
14	A format for databasing and comparison of AFLP fingerprint profiles. BMC Bioinformatics, 2003, 4, 7.	2.6	20
15	Visual Opsin Diversity in Sharks and Rays. Molecular Biology and Evolution, 2020, 37, 811-827.	8.9	20
16	Whole Exome Sequencing of Extreme Morbid Obesity Patients: Translational Implications for Obesity and Related Disorders. Genes, 2014, 5, 709-725.	2.4	19
17	Transcriptome Sequencing of Two Phenotypic Mosaic Eucalyptus Trees Reveals Large Scale Transcriptome Re-Modelling. PLoS ONE, 2015, 10, e0123226.	2.5	18
18	Systems-guided forward genetic screen reveals a critical role of the replication stress response protein ETAA1 in T cell clonal expansion. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, E5216-E5225.	7.1	18

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19	Species trees from consensus single nucleotide polymorphism (SNP) data: Testing phylogenetic approaches with simulated and empirical data. Molecular Phylogenetics and Evolution, 2017, 116, 192-201.	2.7	16
20	Transcriptome Profiling of <i>Melaleuca quinquenervia</i> Challenged by Myrtle Rust Reveals Differences in Defense Responses Among Resistant Individuals. Phytopathology, 2018, 108, 495-509.	2.2	16
21	FluoMEP: A new genotyping method combining the advantages of randomly amplified polymorphic DNA and amplified fragment length polymorphism. Electrophoresis, 2007, 28, 525-534.	2.4	14
22	Evolution of the shut-off steps of vertebrate phototransduction. Open Biology, 2018, 8, 170232.	3.6	10
23	Genotyping of whole genome amplified reduced representation libraries reveals a cryptic population of Culicoides brevitarsis in the Northern Territory, Australia. BMC Genomics, 2016, 17, 769.	2.8	9
24	Dynamic Interplay of Innate and Adaptive Immunity During Sterile Retinal Inflammation: Insights From the Transcriptome. Frontiers in Immunology, 2018, 9, 1666.	4.8	8
25	Recurrent miscalling of missense variation from short-read genome sequence data. BMC Genomics, 2019, 20, 546.	2.8	8
26	Machine Learning Improves Upon Clinicians' Prediction of End Stage Kidney Disease. Frontiers in Medicine, 2022, 9, 837232.	2.6	5
27	Increased burden of rare variants in genes of the endosomal Toll-like receptor pathway in patients with systemic lupus erythematosus. Lupus, 2021, 30, 1756-1763.	1.6	2
28	StabilitySort: assessment of protein stability changes on a genome-wide scale to prioritize potentially pathogenic genetic variation. Bioinformatics, 2022, 38, 4220-4222.	4.1	2
29	Cross validation of pooling/resampling GWAS using the WTCCC data. Molecular Biology and Genetic Engineering, 2015, 3, 1.	0.8	O

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