

# Charles Addo-Quaye

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/7467422/publications.pdf>

Version: 2024-02-01

19  
papers

3,635  
citations

759233

12  
h-index

888059

17  
g-index

21  
all docs

21  
docs citations

21  
times ranked

4914  
citing authors

#	ARTICLE	IF	CITATIONS
1	Systematic prediction of EMS-induced mutations in a sorghum mutant population. <i>Plant Direct</i> , 2022, 6, .	1.9	3
2	Mutation of the nuclear pore complex component, <i>aladin1</i> , disrupts asymmetric cell division in <i>Zea mays</i> (maize). <i>G3: Genes, Genomes, Genetics</i> , 2021, 11, .	1.8	8
3	â€œA reference genome assembly and adaptive trait analysis of <i>Castanea mollissima</i> â€œVanuxem,â€™ a source of resistance to chestnut blight in restoration breedingâ€•. <i>Tree Genetics and Genomes</i> , 2020, 16, 1.	1.6	14
4	Mutations in sorghum <i>SBEIIb</i> and <i>SSIIa</i> affect alkali spreading value, starch composition, thermal properties and flour viscosity. <i>Theoretical and Applied Genetics</i> , 2019, 132, 3357-3374.	3.6	5
5	Whole-Genome Sequence Accuracy Is Improved by Replication in a Population of Mutagenized Sorghum. <i>G3: Genes, Genomes, Genetics</i> , 2018, 8, 1079-1094.	1.8	33
6	New Alleles of <i>FAD3A</i> Lower the Linolenic Acid Content of Soybean Seeds. <i>Crop Science</i> , 2018, 58, 713-718.	1.8	18
7	Forward Genetics by Sequencing EMS Variation-Induced Inbred Lines. <i>G3: Genes, Genomes, Genetics</i> , 2017, 7, 413-425.	1.8	33
8	Genome-wide association study identifies a major gene for beech bark disease resistance in American beech ( <i>Fagus grandifolia</i> Ehrh.). <i>BMC Genomics</i> , 2017, 18, 547.	2.8	15
9	miRNA-mediated auxin signalling repression during <i>Vat</i> -mediated aphid resistance in <i>Cucumis melo</i> . <i>Plant, Cell and Environment</i> , 2016, 39, 1216-1227.	5.7	34
10	Re-Evaluation of Reportedly Metal Tolerant <i>Arabidopsis thaliana</i> Accessions. <i>PLoS ONE</i> , 2016, 11, e0130679.	2.5	7
11	Expression of Small RNA in <i>Aphis gossypii</i> and Its Potential Role in the Resistance Interaction with Melon. <i>PLoS ONE</i> , 2012, 7, e48579.	2.5	40
12	Transcriptome-wide identification of microRNA targets in rice. <i>Plant Journal</i> , 2010, 62, 742-759.	5.7	370
13	Sliced microRNA targets and precise loop-first processing of <i>MIR319</i> hairpins revealed by analysis of the <i>Physcomitrella patens</i> degradome. <i>Rna</i> , 2009, 15, 2112-2121.	3.5	186
14	CleaveLand: a pipeline for using degradome data to find cleaved small RNA targets. <i>Bioinformatics</i> , 2009, 25, 130-131.	4.1	642
15	Endogenous siRNA and miRNA Targets Identified by Sequencing of the <i>Arabidopsis</i> Degradome. <i>Current Biology</i> , 2008, 18, 758-762.	3.9	749
16	<i>Physcomitrella patens</i> DCL3 Is Required for 22â€œ24 nt siRNA Accumulation, Suppression of Retrotransposon-Derived Transcripts, and Normal Development. <i>PLoS Genetics</i> , 2008, 4, e1000314.	3.5	68
17	Evolutionary and Biomedical Insights from the Rhesus Macaque Genome. <i>Science</i> , 2007, 316, 222-234.	12.6	1,283
18	Thermal-aware IP virtualization and placement for networks-on-chip architecture. , 0, , .		54

#	ARTICLE	IF	CITATIONS
19	Thermal-Aware Floorplanning Using Genetic Algorithms. , 0, , .		73