

Sarwar Azam

List of Publications by Year in descending order

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15
papers

2,527
citations

759233

12
h-index

996975

15
g-index

15
all docs

15
docs citations

15
times ranked

2673
citing authors

#	ARTICLE	IF	CITATIONS
1	Draft genome sequence of chickpea (<i>Cicer arietinum</i>) provides a resource for trait improvement. <i>Nature Biotechnology</i> , 2013, 31, 240-246.	17.5	1,049
2	Draft genome sequence of pigeonpea (<i>Cajanus cajan</i>), an orphan legume crop of resource-poor farmers. <i>Nature Biotechnology</i> , 2012, 30, 83-89.	17.5	788
3	Genotyping-by-sequencing based intra-specific genetic map refines a QTL-hotspot region for drought tolerance in chickpea. <i>Molecular Genetics and Genomics</i> , 2015, 290, 559-571.	2.1	180
4	High-Throughput SNP Discovery and Genotyping for Constructing a Saturated Linkage Map of Chickpea (<i>Cicer arietinum</i> L.). <i>DNA Research</i> , 2012, 19, 357-373.	3.4	137
5	Comprehensive Transcriptome Assembly of Chickpea (<i>Cicer arietinum</i> L.) Using Sanger and Next Generation Sequencing Platforms: Development and Applications. <i>PLoS ONE</i> , 2014, 9, e86039.	2.5	87
6	Candidate gene analysis for determinacy in pigeonpea (<i>Cajanus</i> spp.). <i>Theoretical and Applied Genetics</i> , 2014, 127, 2663-2678.	3.6	59
7	A chromosomal genomics approach to assess and validate the <i>desi</i> and <i>kabuli</i> draft chickpea genome assemblies. <i>Plant Biotechnology Journal</i> , 2014, 12, 778-786.	8.3	54
8	Integrated physical, genetic and genome map of chickpea (<i>Cicer arietinum</i> L.). <i>Functional and Integrative Genomics</i> , 2014, 14, 59-73.	3.5	49
9	Coverage-based consensus calling (CbCC) of short sequence reads and comparison of CbCC results to identify SNPs in chickpea (<i>Cicer arietinum</i> ; Fabaceae), a crop species without a reference genome. <i>American Journal of Botany</i> , 2012, 99, 186-192.	1.7	34
10	Leptospira surface adhesin (Lsa21) induces Toll like receptor 2 and 4 mediated inflammatory responses in macrophages. <i>Scientific Reports</i> , 2016, 6, 39530.	3.3	23
11	Genome-guided insights reveal organophosphate-degrading <i>Brevundimonas diminuta</i> as <i>Sphingopyxis wildii</i> and define its versatile metabolic capabilities and environmental adaptations. <i>Genome Biology and Evolution</i> , 2017, 9, evw275.	2.5	19
12	Comparative sequence analysis of nitrogen fixation-related genes in six legumes. <i>Frontiers in Plant Science</i> , 2013, 4, 300.	3.6	14
13	Genetic Characterization and Comparative Genome Analysis of <i>Brucella melitensis</i> Isolates from India. <i>International Journal of Genomics</i> , 2016, 2016, 1-13.	1.6	12
14	Genome Organization and Adaptive Potential of Archetypal Organophosphate Degrading <i>Sphingobium fuliginis</i> ATCC 27551. <i>Genome Biology and Evolution</i> , 2019, 11, 2557-2562.	2.5	12
15	An Integrated SNP Mining and Utilization (ISMU) Pipeline for Next Generation Sequencing Data. <i>PLoS ONE</i> , 2014, 9, e101754.	2.5	10