

# Aamir W Khan

## List of Publications by Year in descending order

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Version: 2024-02-01

40  
papers

3,634  
citations

159525

30  
h-index

302012

39  
g-index

41  
all docs

41  
docs citations

41  
times ranked

2937  
citing authors

#	ARTICLE	IF	CITATIONS
1	Chromosome-length genome assemblies of six legume species provide insights into genome organization, evolution, and agronomic traits for crop improvement. <i>Journal of Advanced Research</i> , 2022, 42, 315-329.	4.4	20
2	QTL-seq for the identification of candidate genes for days to flowering and leaf shape in pigeonpea. <i>Heredity</i> , 2022, 128, 411-419.	1.2	9
3	Genetic variation in <i>CaTIFY4b</i> contributes to drought adaptation in chickpea. <i>Plant Biotechnology Journal</i> , 2022, 20, 1701-1715.	4.1	23
4	A diagnostic marker kit for Fusarium wilt and sterility mosaic diseases resistance in pigeonpea. <i>Theoretical and Applied Genetics</i> , 2021, 134, 367-379.	1.8	10
5	MutMap Approach Enables Rapid Identification of Candidate Genes and Development of Markers Associated With Early Flowering and Enhanced Seed Size in Chickpea ( <i>Cicer arietinum</i> L.). <i>Frontiers in Plant Science</i> , 2021, 12, 688694.	1.7	7
6	Characterization of heterosis and genomic prediction-based establishment of heterotic patterns for developing better hybrids in pigeonpea. <i>Plant Genome</i> , 2021, 14, e20125.	1.6	6
7	A chickpea genetic variation map based on the sequencing of 3,366 genomes. <i>Nature</i> , 2021, 599, 622-627.	13.7	106
8	Whole-genome resequencing-based QTL-seq identified candidate genes and molecular markers for fresh seed dormancy in groundnut. <i>Plant Biotechnology Journal</i> , 2020, 18, 992-1003.	4.1	60
9	Genome-wide analysis of epigenetic and transcriptional changes associated with heterosis in pigeonpea. <i>Plant Biotechnology Journal</i> , 2020, 18, 1697-1710.	4.1	38
10	Super-Pangenome by Integrating the Wild Side of a Species for Accelerated Crop Improvement. <i>Trends in Plant Science</i> , 2020, 25, 148-158.	4.3	177
11	Superior haplotypes for haplotype-based breeding for drought tolerance in pigeonpea ( <i>Cajanus</i> Tj ETQq1 1 0.784314 rgBT /Overlo	4.1	81
12	<i>Arachis hypogaea</i> gene expression atlas for <i>fastigiata</i> subspecies of cultivated groundnut to accelerate functional and translational genomics applications. <i>Plant Biotechnology Journal</i> , 2020, 18, 2187-2200.	4.1	38
13	Trait associations in the pangenome of pigeon pea ( <i>Cajanus cajan</i> ). <i>Plant Biotechnology Journal</i> , 2020, 18, 1946-1954.	4.1	79
14	Next-generation sequencing identified genomic region and diagnostic markers for resistance to bacterial wilt on chromosome B02 in peanut ( <i>Arachis hypogaea</i> L.). <i>Plant Biotechnology Journal</i> , 2019, 17, 2356-2369.	4.1	41
15	Resequencing of 429 chickpea accessions from 45 countries provides insights into genome diversity, domestication and agronomic traits. <i>Nature Genetics</i> , 2019, 51, 857-864.	9.4	219
16	The genome of cultivated peanut provides insight into legume karyotypes, polyploid evolution and crop domestication. <i>Nature Genetics</i> , 2019, 51, 865-876.	9.4	398
17	Discovery of genomic regions and candidate genes controlling shelling percentage using QTL-seq approach in cultivated peanut ( <i>Arachis hypogaea</i> L.). <i>Plant Biotechnology Journal</i> , 2019, 17, 1248-1260.	4.1	51
18	Integrated transcriptome, small RNA and degradome sequencing approaches provide insights into Ascochyta blight resistance in chickpea. <i>Plant Biotechnology Journal</i> , 2019, 17, 914-931.	4.1	66

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19	Development and Application of High-Density Axiom <i>Cajanus</i> SNP Array with 56K SNPs to Understand the Genome Architecture of Released Cultivars and Founder Genotypes. <i>Plant Genome</i> , 2018, 11, 180005.	1.6	35
20	Molecular Mapping of QTLs for Heat Tolerance in Chickpea. <i>International Journal of Molecular Sciences</i> , 2018, 19, 2166.	1.8	73
21	Whole-genome resequencing of 292 pigeonpea accessions identifies genomic regions associated with domestication and agronomic traits. <i>Nature Genetics</i> , 2017, 49, 1082-1088.	9.4	218
22	Indel-seq: a fast-forward genetics approach for identification of trait-associated putative candidate genomic regions and its application in pigeonpea ( <i>Cajanus cajan</i> ). <i>Plant Biotechnology Journal</i> , 2017, 15, 906-914.	4.1	67
23	QTL-seq approach identified genomic regions and diagnostic markers for rust and late leaf spot resistance in groundnut ( <i>Arachis hypogaea</i> ). <i>Plant Biotechnology Journal</i> , 2017, 15, 927-941.	4.1	198
24	Sequencing the Chickpea Genome. <i>Compendium of Plant Genomes</i> , 2017, , 117-123.	0.3	0
25	Genome-Wide Identification, Characterization, and Expression Analysis of Small RNA Biogenesis Purveyors Reveal Their Role in Regulation of Biotic Stress Responses in Three Legume Crops. <i>Frontiers in Plant Science</i> , 2017, 8, 488.	1.7	15
26	Molecular Mapping of Flowering Time Major Genes and QTLs in Chickpea ( <i>Cicer arietinum</i> L.). <i>Frontiers in Plant Science</i> , 2017, 8, 1140.	1.7	48
27	QTL-seq for rapid identification of candidate genes for 100-seed weight and root/total plant dry weight ratio under rainfed conditions in chickpea. <i>Plant Biotechnology Journal</i> , 2016, 14, 2110-2119.	4.1	177
28	First-generation HapMap in <i>Cajanus</i> spp. reveals untapped variations in parental lines of mapping populations. <i>Plant Biotechnology Journal</i> , 2016, 14, 1673-1681.	4.1	39
29	Genome-wide dissection of AP2/ERF and HSP90 gene families in five legumes and expression profiles in chickpea and pigeonpea. <i>Plant Biotechnology Journal</i> , 2016, 14, 1563-1577.	4.1	109
30	Next-generation sequencing for identification of candidate genes for <i>Fusarium</i> wilt and sterility mosaic disease in pigeonpea ( <i>Cajanus cajan</i> ). <i>Plant Biotechnology Journal</i> , 2016, 14, 1183-1194.	4.1	108
31	Draft genome of the peanut A-genome progenitor ( <i>Arachis duranensis</i> ) provides insights into geocarpy, oil biosynthesis, and allergens. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 6785-6790.	3.3	235
32	Whole genome re-sequencing reveals genome-wide variations among parental lines of 16 mapping populations in chickpea ( <i>Cicer arietinum</i> L.). <i>BMC Plant Biology</i> , 2016, 16, 10.	1.6	101
33	Association of nad7a Gene with Cytoplasmic Male Sterility in Pigeonpea. <i>Plant Genome</i> , 2015, 8, eplantgenome2014.11.0084.	1.6	28
34	CicArVarDB: SNP and InDel database for advancing genetics research and breeding applications in chickpea. <i>Database: the Journal of Biological Databases and Curation</i> , 2015, 2015, bav078.	1.4	22
35	Identification and Validation of Selected Universal Stress Protein Domain Containing Drought-Responsive Genes in Pigeonpea ( <i>Cajanus cajan</i> L.). <i>Frontiers in Plant Science</i> , 2015, 6, 1065.	1.7	39
36	NGS-QCbox and Raspberry for Parallel, Automated and Rapid Quality Control Analysis of Large-Scale Next Generation Sequencing (Illumina) Data. <i>PLoS ONE</i> , 2015, 10, e0139868.	1.1	37

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37	Genomewide Association Studies for 50 Agronomic Traits in Peanut Using the "Reference Set"™ Comprising 300 Genotypes from 48 Countries of the Semi-Arid Tropics of the World. PLoS ONE, 2014, 9, e105228.	1.1	124
38	CicArMiSatDB: the chickpea microsatellite database. BMC Bioinformatics, 2014, 15, 212.	1.2	33
39	A draft genome sequence of the pulse crop chickpea ( <i>Cicer arietinum</i> L.). Plant Journal, 2013, 74, 715-729.	2.8	382
40	High-Throughput SNP Discovery and Genotyping for Constructing a Saturated Linkage Map of Chickpea ( <i>Cicer arietinum</i> L.). DNA Research, 2012, 19, 357-373.	1.5	137