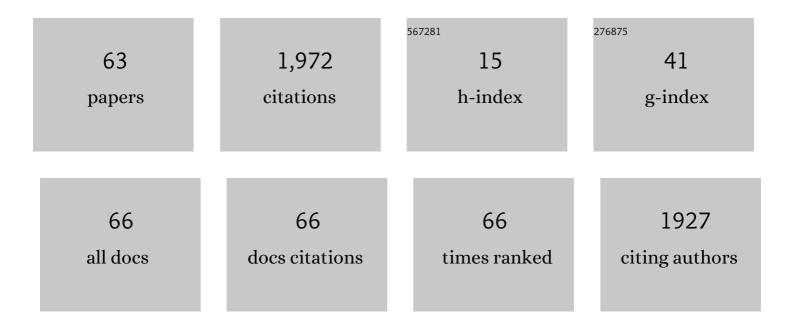
Ibrokhim Y Abdurakhmonov

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/2185398/publications.pdf Version: 2024-02-01



#	Article	IF	CITATIONS
1	Toward Sequencing Cotton (<i>Gossypium</i>) Genomes: Figure 1 Plant Physiology, 2007, 145, 1303-1310.	4.8	390
2	Application of Association Mapping to Understanding the Genetic Diversity of Plant Germplasm Resources. International Journal of Plant Genomics, 2008, 2008, 1-18.	2.2	221
3	Wild Relatives of Maize, Rice, Cotton, and Soybean: Treasure Troves for Tolerance to Biotic and Abiotic Stresses. Frontiers in Plant Science, 2018, 9, 886.	3.6	211
4	Molecular diversity and association mapping of fiber quality traits in exotic G. hirsutum L. germplasm. Genomics, 2008, 92, 478-487.	2.9	179
5	Linkage disequilibrium based association mapping of fiber quality traits in G. hirsutum L. variety germplasm. Genetica, 2009, 136, 401-417.	1.1	144
6	Status of the Global Cotton Germplasm Resources. Crop Science, 2010, 50, 1161-1179.	1.8	115
7	Genome Editing in Plants: An Overview of Tools and Applications. International Journal of Agronomy, 2017, 2017, 1-15.	1.2	82
8	Microsatellite markers associated with lint percentage trait in cotton, Gossypium hirsutum. Euphytica, 2007, 156, 141-156.	1.2	57
9	Phytochrome RNAi enhances major fibre quality and agronomic traits of the cotton Gossypium hirsutum L. Nature Communications, 2014, 5, 3062.	12.8	51
10	Small RNA regulation of ovule development in the cotton plant, G. hirsutum L. BMC Plant Biology, 2008, 8, 93.	3.6	37
11	Genetic diversity and population structure of cotton (<i>Gossypium</i> spp.) of the New World assessed by SSR markers. Botany, 2013, 91, 251-259.	1.0	37
12	RNA Interference for Functional Genomics and Improvement of Cotton (Gossypium sp.). Frontiers in Plant Science, 2016, 7, 202.	3.6	36
13	Genetic Diversity, QTL Mapping, and Marker-Assisted Selection Technology in Cotton (Gossypium spp.). Frontiers in Plant Science, 2021, 12, 779386.	3.6	29
14	Simple Sequence Repeat Marker Associated with a Natural Leaf Defoliation Trait in Tetraploid Cotton. Journal of Heredity, 2005, 96, 644-653.	2.4	21
15	Role of MicroRNAs and small RNAs in regulation of developmental processes and agronomic traits in Gossypium species. Genomics, 2019, 111, 1018-1025.	2.9	19
16	The Role of Induced Mutation in Conversion of Photoperiod Dependence in Cotton. Journal of Heredity, 2007, 98, 258-266.	2.4	18
17	Molecular confirmation of Gossypium hirsutum chromosome substitution lines. Euphytica, 2015, 205, 459-473.	1.2	17

18 Genomics-Assisted Plant Breeding in the 21st Century: Technological Advances and Progress. , 0, , .

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#	Article	IF	CITATIONS
19	Development, genetic mapping and QTL association of cotton PHYA, PHYB, and HY5-specific CAPS and dCAPS markers. BMC Genetics, 2016, 17, 141.	2.7	15
20	Genetic diversity, linkage disequilibrium, and association mapping analyses of Gossypium barbadense L. germplasm. PLoS ONE, 2017, 12, e0188125.	2.5	15
21	Chitin-binding antifungal protein from Ficus carica latex. Chemistry of Natural Compounds, 2008, 44, 216-219.	0.8	14
22	Solid-Phase Colorimetric Method for the Quantification of Fucoidan. Applied Biochemistry and Biotechnology, 2012, 168, 1019-1024.	2.9	12
23	Duplication, divergence and persistence in the Phytochrome photoreceptor gene family of cottons (Gossypium spp.). BMC Plant Biology, 2010, 10, 119.	3.6	11
24	Genetic Diversity in Gossypium genus. , 0, , .		11
25	Genomics Era for Plants and Crop Species $\hat{a} \in$ "Advances Made and Needed Tasks Ahead. , 0, , .		11
26	QTL mapping for flowering-time and photoperiod insensitivity of cotton Gossypium darwinii Watt. PLoS ONE, 2017, 12, e0186240.	2.5	11
27	World Cotton Germplasm Resources. , 2014, , .		11
28	Molecular Characterization of Uzbekistan Isolates of Fusarium oxysporum f. sp. vasinfectum. Journal of Plant Science and Molecular Breeding, 2013, 2, 3.	1.2	11
29	Methodologies for In Vitro Cloning of Small RNAs and Application for Plant Genome(s). International Journal of Plant Genomics, 2009, 2009, 1-13.	2.2	10
30	Clustering, haplotype diversity and locations of MIC-3: a unique root-specific defense-related gene family in Upland cotton (Gossypium hirsutum L.). Theoretical and Applied Genetics, 2010, 120, 587-606.	3.6	10
31	Bioinformatics: Basics, Development, and Future. , 0, , .		10
32	Genome-wide identification and characterization of microRNAs differentially expressed in fibers in a cotton phytochrome A1 RNAi line. PLoS ONE, 2017, 12, e0179381.	2.5	9
33	Introduction to Microsatellites: Basics, Trends and Highlights. , 0, , .		8
34	Functional intron-derived miRNAs and host-gene expression in plants. Plant Methods, 2018, 14, 83.	4.3	8
35	Transcriptome Analysis of Ten-DPA Fiber in an Upland Cotton (<i>Gossypium) Tj ETQq1 1 0.7843 American Journal of Plant Sciences, 2017, 08, 2530-2553.</i>	0.8 0.8	Overlock 10 8
36	Chromosome Substitution Lines: Concept, Development and Utilization in the Genetic Improvement of Upland Cotton. , 0, , .		7

#	Article	IF	CITATIONS
37	Profiling of the most reliable mutations from sequenced SARS-CoV-2 genomes scattered in Uzbekistan. PLoS ONE, 2022, 17, e0266417.	2.5	7
38	Registration of three <i>Gossypium barbadense</i> L. American pimaâ€like germplasm lines (PSSJâ€FRP01,) Tj ET Journal of Plant Registrations, 2022, 16, 626-634.	[Qq0 0 0 r 0.5	gBT /Overloo 7
39	Cytogenetic Characteristics of New Monosomic Stocks of Cotton (Gossypium hirsutum L.). Genetics Research International, 2011, 2011, 1-12.	2.0	6
40	Detection of <i>Fusarium oxysporum</i> f. sp. v <i>asinfectum</i> race 3 by single-base extension method and allele-specific polymerase chain reaction. Canadian Journal of Plant Pathology, 2014, 36, 216-223.	1.4	6
41	Analyses of Fusarium wilt race 3 resistance in Upland cotton (Gossypium hirsutum L.). Genetica, 2015, 143, 385-392.	1.1	5
42	Morphological characteristics and identification of new monosomic stocks for cotton (Gossypium) Tj ETQq0 0 0	rgBT_/Ove	rloçk 10 Tf 5
43	Cotton Breeding in the View of Abiotic and Biotic Stresses: Challenges and Perspectives. , 0, , .		5
44	Development of Superior Fibre Quality Upland Cotton Cultivar Series †Ravnaq' Using Marker-Assisted Selection. Frontiers in Plant Science, 2022, 13, .	3.6	5
45	Molecular evolution of the clustered MIC-3 multigene family of Gossypium species. Theoretical and Applied Genetics, 2011, 123, 1359-1373.	3.6	4
46	Characterization of Small RNAs and Their Targets from Fusarium oxysporum Infected and Noninfected Cotton Root Tissues. Plant Molecular Biology Reporter, 2016, 34, 698-706.	1.8	4
47	Cotton Germplasm Collection of Uzbekistan. , 0, , .		4
48	Bioinformatics - Updated Features and Applications. , 2016, , .		4
49	Genome sequence diversity of SARS-CoV-2 obtained from clinical samples in Uzbekistan. PLoS ONE, 2022, 17, e0270314.	2.5	4
50	RNA Interference $\hat{a} \in \hat{~}$ A Hallmark of Cellular Function and Gene Manipulation. , 0, , .		3
51	Introductory Chapter: Introduction to Cotton Research Highlights. , 0, , .		3
52	Comparative assessment of genetic diversity in cytoplasmic and nuclear genome of upland cotton. Genetica, 2016, 144, 289-306.	1.1	3
53	A High-Throughput Standard PCR-Based Genotyping Method for Determining Transgene Zygosity in Segregating Plant Populations. Frontiers in Plant Science, 2017, 8, 1252.	3.6	3

Recent Developments in Fiber Genomics of Tetraploid Cotton Species. , 2018, , .

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#	Article	IF	CITATIONS
55	Alteration of root and shoot morphologies by interspecific replacement of individual Upland cotton chromosome segment pairs. Euphytica, 2021, 217, 1.	1.2	3
56	The Cotton-Insect Interactive Transcriptome $\hat{a} {\in} ``$ Molecular Elements Involved in Plant-Insect Interactions. , 2018, , 62-73.		2
57	Transcriptome Analysis of Ten Days Post Anthesis Elongating Fiber in the Upland Cotton (<i>Gossypium hirsutum</i>) Chromosome Substitution Line CS-B25. American Journal of Plant Sciences, 2018, 09, 1334-1361.	0.8	2
58	Low molecular fucoidan and its macromolecular complex with bee venom melittin. Advances in Bioscience and Biotechnology (Print), 2011, 02, 298-303.	0.7	1
59	Using of Genome Editing Methods in Plant Breeding. , 0, , .		1
60	Cotton as a Model for Polyploidy and Fiber Development Study. , 0, , .		1
61	Gene Flow at the Crossroads of Humanity: mtDNA Sequence Diversity and Alu Insertion Polymorphism Frequencies in Uzbekistan. The Open Genomics Journal, 2009, 2, 1-11.	0.5	1
62	Overview of the Biosafety and Risk Assessment Steps for Insect-resistant Biotech Crops. , 2018, , 178-203.		1
63	Introductory Chapter: Global Cotton Research Development Trends for the Past Five Years - Key Directions. , 0, , .		Ο