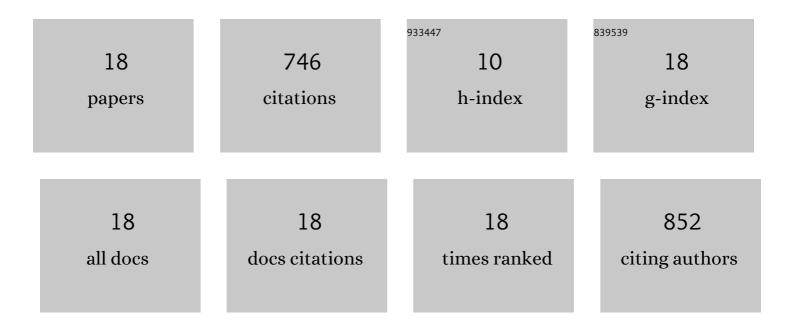


## List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	Persistent whole-chromosome aneuploidy is generally associated with nascent allohexaploid wheat. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 3447-3452.	7.1	180
2	Molecular Cytogenetic Characterization of Wheat–Thinopyrum elongatum Addition, Substitution and Translocation Lines with a Novel Source of Resistance to Wheat Fusarium Head Blight. Journal of Genetics and Genomics, 2012, 39, 103-110.	3.9	90
3	Intrinsic karyotype stability and gene copy number variations may have laid the foundation for tetraploid wheat formation. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 19466-19471.	7.1	79
4	Evolution of the BBAA Component of Bread Wheat during Its History at the Allohexaploid Level. Plant Cell, 2014, 26, 2761-2776.	6.6	77
5	Global transgenerational gene expression dynamics in two newly synthesized allohexaploid wheat (Triticum aestivum) lines. BMC Biology, 2012, 10, 3.	3.8	75
6	Extensive and Heritable Epigenetic Remodeling and Genetic Stability Accompany Allohexaploidization of Wheat. Genetics, 2011, 188, 499-510.	2.9	72
7	Rapid genomic changes in polyploid wheat and related species: implications for genome evolution and genetic improvement. Journal of Genetics and Genomics, 2009, 36, 519-528.	3.9	54
8	Chromosomal and genome-wide molecular changes associated with initial stages of allohexaploidization in wheat can be transit and incidental. Genome, 2011, 54, 692-699.	2.0	38
9	Tissue culture-induced variation at simple sequence repeats in sorghum (Sorghum bicolor L.) is genotype-dependent and associated with down-regulated expression of a mismatch repair gene, MLH3. Plant Cell Reports, 2010, 29, 51-59.	5.6	20
10	Generality and characteristics of genetic and epigenetic changes in newly synthesized allotetraploid wheat lines. Journal of Genetics and Genomics, 2010, 37, 737-748.	3.9	15
11	The fungal community in non-rhizosphere soil of <i> Panax ginseng</i> are driven by different cultivation modes and increased cultivation periods. PeerJ, 2020, 8, e9930.	2.0	10
12	Dramatic genotypic difference in, and effect of genetic crossing on, tissue culture-induced mobility of retrotransposon Tos17 in rice. Plant Cell Reports, 2012, 31, 2057-2063.	5.6	9
13	Enzymatic gene expression by Pleurotus tuoliensis (Bailinggu): differential regulation under low temperature induction conditions. World Journal of Microbiology and Biotechnology, 2018, 34, 160.	3.6	9
14	Transcriptome Changes during Major Developmental Transitions Accompanied with Little Alteration of DNA Methylome in Two Pleurotus Species. Genes, 2019, 10, 465.	2.4	8
15	DNA Methylation Changes in Pleurotus eryngii Subsp. tuoliensis (Bailinggu) in Response to Low Temperature Stress. International Journal of Agriculture and Biology, 2017, 19, 328-334.	0.4	4
16	Characterization of copia retrotransposons in Zizania latifolia shows atypical cytosine methylation patterns and differential occurrence from other species of the grass family. Aquatic Botany, 2009, 90, 213-221.	1.6	2
17	Design of potentially universal SSU primers in myxomycetes using next-generation sequencing. Journal of Microbiological Methods, 2021, 184, 106203.	1.6	2
18	Morphological and molecular characterization of the new aethaloid species <i>Didymium yulii</i> . Mycologia, 2021, 113, 1-12.	1.9	2