

# Naeem H Syed

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/9117407/publications.pdf>

Version: 2024-02-01

18  
papers

1,540  
citations

759233

12  
h-index

839539

18  
g-index

18  
all docs

18  
docs citations

18  
times ranked

2180  
citing authors

#	ARTICLE	IF	CITATIONS
1	Alternative splicing in plants “coming of age. Trends in Plant Science, 2012, 17, 616-623.	8.8	464
2	Alternative splicing and nonsense-mediated decay modulate expression of important regulatory genes in Arabidopsis. Nucleic Acids Research, 2012, 40, 2454-2469.	14.5	439
3	Alternative Splicing and Protein Diversity: Plants Versus Animals. Frontiers in Plant Science, 2019, 10, 708.	3.6	136
4	Perspective on Alternative Splicing and Proteome Complexity in Plants. Trends in Plant Science, 2019, 24, 496-506.	8.8	129
5	Does co-transcriptional regulation of alternative splicing mediate plant stress responses?. Nucleic Acids Research, 2019, 47, 2716-2726.	14.5	86
6	Comparative analysis of the drought-responsive transcriptome in soybean lines contrasting for canopy wilting. Plant Science, 2015, 240, 65-78.	3.6	53
7	A detailed linkage map of lettuce based on SSAP, AFLP and NBS markers. Theoretical and Applied Genetics, 2006, 112, 517-527.	3.6	52
8	Core clock, <i>SUB1</i> , and <i>ABAR</i> genes mediate flooding and drought responses via alternative splicing in soybean. Journal of Experimental Botany, 2015, 66, 7129-7149.	4.8	52
9	Sequence-specific amplification polymorphisms (SSAPs): a multi-locus approach for analyzing transposon insertions. Nature Protocols, 2006, 1, 2746-2752.	12.0	48
10	Genome-Wide Identification of Splicing Quantitative Trait Loci (sQTLs) in Diverse Ecotypes of Arabidopsis thaliana. Frontiers in Plant Science, 2019, 10, 1160.	3.6	19
11	Differential nucleosome occupancy modulates alternative splicing in <i>Arabidopsis thaliana</i> . New Phytologist, 2021, 229, 1937-1945.	7.3	19
12	Targeting DNA methyltransferases in non-small-cell lung cancer. Seminars in Cancer Biology, 2022, 83, 77-87.	9.6	13
13	Decoding co-/post-transcriptional complexities of plant transcriptomes and epitranscriptome using next-generation sequencing technologies. Biochemical Society Transactions, 2020, 48, 2399-2414.	3.4	9
14	Genome-Tagged Amplification (GTA): a PCR-based method to prepare sample-tagged amplicons from hundreds of individuals for next generation sequencing. Molecular Breeding, 2014, 34, 977-988.	2.1	7
15	Development of retrotransposon-based SSAP molecular marker system for study of genetic diversity in sea holly ( <i>Eryngium maritimum</i> L.). Plant Genetic Resources: Characterisation and Utilisation, 2010, 8, 258-266.	0.8	6
16	Epigenetic differences in an identical genetic background modulate alternative splicing in <i>A. thaliana</i> . Genomics, 2021, 113, 3476-3486.	2.9	5
17	Stochastic Variation in DNA Methylation Modulates Nucleosome Occupancy and Alternative Splicing in Arabidopsis thaliana. Plants, 2022, 11, 1105.	3.5	2
18	Genetic Diversity and Structure of Northern Populations of the Declining Coastal Plant <i>Eryngium maritimum</i> . Proceedings of the Latvian Academy of Sciences, 2019, 73, 446-454.	0.1	1