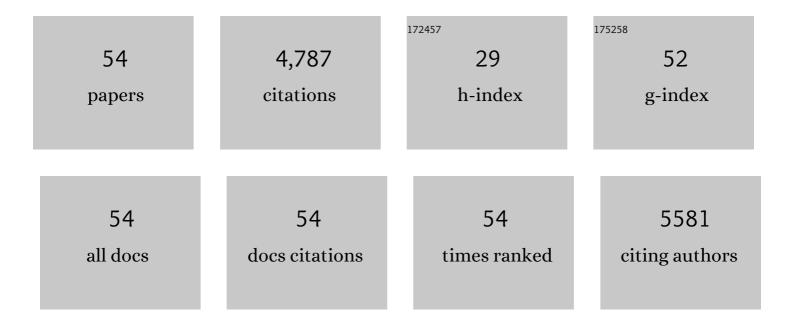
## Anireddy S N Reddy

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	Complexity of the Alternative Splicing Landscape in Plants  Â. Plant Cell, 2013, 25, 3657-3683.	6.6	731
2	Coping with Stresses: Roles of Calcium- and Calcium/Calmodulin-Regulated Gene Expression Â. Plant Cell, 2011, 23, 2010-2032.	6.6	624
3	A survey of the sorghum transcriptome using single-molecule long reads. Nature Communications, 2016, 7, 11706.	12.8	496
4	Alternative Splicing of Pre-Messenger RNAs in Plants in the Genomic Era. Annual Review of Plant Biology, 2007, 58, 267-294.	18.7	465
5	Alternative Splicing and Protein Diversity: Plants Versus Animals. Frontiers in Plant Science, 2019, 10, 708.	3.6	136
6	Perspective on Alternative Splicing and Proteome Complexity in Plants. Trends in Plant Science, 2019, 24, 496-506.	8.8	129
7	Analysis of Transcriptome and Epitranscriptome in Plants Using PacBio Iso-Seq and Nanopore-Based Direct RNA Sequencing. Frontiers in Genetics, 2019, 10, 253.	2.3	127
8	Abiotic Stresses Modulate Landscape of Poplar Transcriptome via Alternative Splicing, Differential Intron Retention, and Isoform Ratio Switching. Frontiers in Plant Science, 2018, 9, 5.	3.6	122
9	Development of an in vitro pre-mRNA splicing assay using plant nuclear extract. Plant Methods, 2018, 14, 1.	4.3	121
10	Plant serine/arginineâ€rich proteins: roles in precursor messenger RNA splicing, plant development, and stress responses. Wiley Interdisciplinary Reviews RNA, 2011, 2, 875-889.	6.4	111
11	The Kinesin-like Calmodulin Binding Protein Is Differentially Involved in Cell Division. Plant Cell, 2000, 12, 979-990.	6.6	110
12	Transcriptome-Wide Identification of RNA Targets of Arabidopsis SERINE/ARGININE-RICH45 Uncovers the Unexpected Roles of This RNA Binding Protein in RNA Processing. Plant Cell, 2015, 27, 3294-3308.	6.6	107
13	Characterization of Microtubule Binding Domains in the Arabidopsis Kinesin-like Calmodulin Binding Protein. Plant Cell, 1998, 10, 957-965.	6.6	101
14	Plant serine/arginine-rich proteins and their role in pre-mRNA splicing. Trends in Plant Science, 2004, 9, 541-547.	8.8	97
15	Quantitative profiling of N6-methyladenosine at single-base resolution in stem-differentiating xylem of Populus trichocarpa using Nanopore direct RNA sequencing. Genome Biology, 2021, 22, 22.	8.8	88
16	Does co-transcriptional regulation of alternative splicing mediate plant stress responses?. Nucleic Acids Research, 2019, 47, 2716-2726.	14.5	86
17	Transcriptome Analysis of Drought-Resistant and Drought-Sensitive Sorghum (Sorghum bicolor) Genotypes in Response to PEG-Induced Drought Stress. International Journal of Molecular Sciences, 2020, 21, 772.	4.1	79
18	Deciphering the Plant Splicing Code: Experimental and Computational Approaches for Predicting Alternative Splicing and Splicing Regulatory Elements. Frontiers in Plant Science, 2012, 3, 18.	3.6	78

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19	Organâ€specific, developmental, hormonal and stress regulation of expression of putative pectate lyase genes in Arabidopsis. New Phytologist, 2007, 174, 537-550.	7.3	75
20	The Plant U1 Small Nuclear Ribonucleoprotein Particle 70K Protein Interacts with Two Novel Serine/Arginine–Rich Proteins. Plant Cell, 1998, 10, 1637-1647.	6.6	74
21	Localization and Dynamics of Nuclear Speckles in Plants. Plant Physiology, 2012, 158, 67-77.	4.8	74
22	Identification of an intronic splicing regulatory element involved in autoâ€regulation of alternative splicing of <i>SCL33</i> preâ€mRNA. Plant Journal, 2012, 72, 935-946.	5.7	71
23	Exploring the relationship between intron retention and chromatin accessibility in plants. BMC Genomics, 2018, 19, 21.	2.8	61
24	Phytophthora Effectors Modulate Genome-wide Alternative Splicing of Host mRNAs to Reprogram Plant Immunity. Molecular Plant, 2020, 13, 1470-1484.	8.3	49
25	The Arabidopsis splicing regulator SR45 confers salt tolerance in a splice isoform-dependent manner. Plant Molecular Biology, 2019, 100, 379-390.	3.9	46
26	Stress-Induced Changes in Alternative Splicing Landscape in Rice: Functional Significance of Splice Isoforms in Stress Tolerance. Biology, 2021, 10, 309.	2.8	45
27	Global gene expression analysis using RNA-seq uncovered a new role for SR1/CAMTA3 transcription factor in salt stress. Scientific Reports, 2016, 6, 27021.	3.3	37
28	Isolation and Characterization of a Novel Calmodulin-binding Protein from Potato. Journal of Biological Chemistry, 2002, 277, 4206-4214.	3.4	36
29	Profiling of circular RNA N <sup>6</sup> â€methyladenosine in moso bamboo ( <i>Phyllostachys) Tj ETQq1 1 0.784 1823-1838.</i>	1314 rgBT 8.5	/Overlock 1 35
30	Serine/Arginine-rich protein family of splicing regulators: New approaches to study splice isoform functions. Plant Science, 2019, 283, 127-134.	3.6	27
31	Differential Recruitment of Splice Variants from SR Pre-mRNAs to Polysomes During Development and in Response to Stresses. Plant and Cell Physiology, 2015, 56, 421-427.	3.1	24
32	Wideâ€ranging transcriptome remodelling mediated by alternative polyadenylation in response to abiotic stresses in <i>Sorghum</i> . Plant Journal, 2020, 102, 916-930.	5.7	24
33	Multiplex CRISPR Mutagenesis of the Serine/Arginine-Rich (SR) Gene Family in Rice. Genes, 2019, 10, 596.	2.4	23
34	Alternative splicing dynamics and evolutionary divergence during embryogenesis in wheat species. Plant Biotechnology Journal, 2021, 19, 1624-1643.	8.3	23
35	Vascular Plant One-Zinc-Finger (VOZ) Transcription Factors Are Positive Regulators of Salt Tolerance in Arabidopsis. International Journal of Molecular Sciences, 2018, 19, 3731.	4.1	21
36	A Ca2+/CaM-regulated transcriptional switch modulates stomatal development in response to water deficit. Scientific Reports, 2019, 9, 12282.	3.3	19

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37	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
38	Differential nucleosome occupancy modulates alternative splicing in <i>Arabidopsis thaliana</i> . New Phytologist, 2021, 229, 1937-1945.	7.3	19
39	An in-frame deletion mutation in the degron tail of auxin coreceptor <i>IAA2</i> confers resistance to the herbicide 2,4-D in <i>Sisymbrium orientale</i> the Vacceedings of the National Academy of Sciences of the United States of America, 2022, 119, .	7.1	19
40	A pollen-specific calmodulin-binding protein, NPG1, interacts with putative pectate lyases. Scientific Reports, 2014, 4, 5263.	3.3	18
41	The interplay between microRNA and alternative splicing of linear and circular RNAs in eleven plant species. Bioinformatics, 2019, 35, 3119-3126.	4.1	18
42	Drought induces epitranscriptome and proteome changes in stem-differentiating xylem of <i>Populus trichocarpa</i> . Plant Physiology, 2022, 190, 459-479.	4.8	18
43	Production of Phloroglucinol, a Platform Chemical, in Arabidopsis using a Bacterial Gene. Scientific Reports, 2016, 6, 38483.	3.3	17
44	The Landscape of RNA-Protein Interactions in Plants: Approaches and Current Status. International Journal of Molecular Sciences, 2021, 22, 2845.	4.1	17
45	Genomeâ€wide profiling of circular RNAs, alternative splicing, and Râ€loops in stemâ€differentiating xylem of <i>Populus trichocarpa</i> . Journal of Integrative Plant Biology, 2021, 63, 1294-1308.	8.5	14
46	The Rice Serine/Arginine Splicing Factor RS33 Regulates Pre-mRNA Splicing during Abiotic Stress Responses. Cells, 2022, 11, 1796.	4.1	14
47	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
48	Overlapping roles of spliceosomal components SF3B1 and PHF5A in rice splicing regulation. Communications Biology, 2021, 4, 529.	4.4	8
49	Incorporation of gap characters and lineage-specific regions into phylogenetic analyses of gene families from divergent clades: an example from the kinesin superfamily across eukaryotes. Cladistics, 2008, 24, 372-384.	3.3	7
50	Salt-Induced Stability of <i>SR1/CAMTA3</i> mRNA Is Mediated by Reactive Oxygen Species and Requires the 3' End of Its Open Reading Frame. Plant and Cell Physiology, 2020, 61, 748-760.	3.1	7
51	RODAN: a fully convolutional architecture for basecalling nanopore RNA sequencing data. BMC Bioinformatics, 2022, 23, 142.	2.6	7
52	PSDX: A Comprehensive Multi-Omics Association Database of Populus trichocarpa With a Focus on the Secondary Growth in Response to Stresses. Frontiers in Plant Science, 2021, 12, 655565.	3.6	2
53	Analysis of Calcium/Calmodulin Regulation of a Plant Kinesin Using Co-Sedimentation and ATPase Assays. Methods in Molecular Biology, 2007, 392, 23-36.	0.9	2
54	Arabidopsis U1 snRNP 70K protein and its interacting proteins: nuclear localization and in vivo dynamics of a novel plant-specific serine/arginine-rich protein. Symposia of the Society for Experimental Biology, 2004, , 279-95.	0.0	0