

# Linda A Rymarquis

## List of Publications by Year in descending order

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18  
papers

4,085  
citations

567281

15  
h-index

839539

18  
g-index

18  
all docs

18  
docs citations

18  
times ranked

6071  
citing authors

#	ARTICLE	IF	CITATIONS
1	The <i>Chlamydomonas</i> Genome Reveals the Evolution of Key Animal and Plant Functions. <i>Science</i> , 2007, 318, 245-250.	12.6	2,354
2	Global identification of microRNA target RNA pairs by parallel analysis of RNA ends. <i>Nature Biotechnology</i> , 2008, 26, 941-946.	17.5	793
3	Sample sequencing of vascular plants demonstrates widespread conservation and divergence of microRNAs. <i>Nature Communications</i> , 2014, 5, 3722.	12.8	224
4	Uridylation of mature miRNAs and siRNAs by the MUT68 nucleotidyltransferase promotes their degradation in <i>Chlamydomonas</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 3906-3911.	7.1	122
5	Identification of SMC6 cleavage sites and a preferred RNA cleavage motif by global analysis of endogenous NMD targets in human cells. <i>Nucleic Acids Research</i> , 2015, 43, 309-323.	14.5	90
6	Diamonds in the rough: mRNA-like non-coding RNAs. <i>Trends in Plant Science</i> , 2008, 13, 329-334.	8.8	80
7	Evidence that XRN4, an <i>Arabidopsis</i> homolog of exoribonuclease XRN1, preferentially impacts transcripts with certain sequences or in particular functional categories. <i>Rna</i> , 2011, 17, 501-511.	3.5	76
8	Parallel analysis of RNA ends enhances global investigation of microRNAs and target RNAs of <i>Brachypodium distachyon</i> . <i>Genome Biology</i> , 2013, 14, R145.	9.6	67
9	Beyond Complementation. Map-Based Cloning in <i>Chlamydomonas reinhardtii</i> . <i>Plant Physiology</i> , 2005, 137, 557-566.	4.8	61
10	Comprehensive Investigation of MicroRNAs Enhanced by Analysis of Sequence Variants, Expression Patterns, ARGONAUTE Loading, and Target Cleavage. <i>Plant Physiology</i> , 2013, 162, 1225-1245.	4.8	61
11	Adaptive evolution of chloroplast genome structure inferred using a parametric bootstrap approach. <i>BMC Evolutionary Biology</i> , 2006, 6, 13.	3.2	51
12	Abiotic Stress-Associated miRNAs: Detection and Functional Analysis. <i>Methods in Molecular Biology</i> , 2010, 592, 203-230.	0.9	31
13	Porphyra: Complex Life Histories in a Harsh Environment: <i>P. umbilicalis</i> , an Intertidal Red Alga for Genomic Analysis. <i>Cellular Origin and Life in Extreme Habitats</i> , 2010, , 129-148.	0.3	21
14	Nuclear suppressors define three factors that participate in both 5' and 3' end processing of mRNAs in <i>Chlamydomonas</i> chloroplasts. <i>Plant Journal</i> , 2006, 46, 448-461.	5.7	19
15	MAJOR DEVELOPMENTAL REGULATORS AND THEIR EXPRESSION IN TWO CLOSELY RELATED SPECIES OF <i>PORPHYRA</i> (RHODOPHYTA). <i>Journal of Phycology</i> , 2012, 48, 883-896.	2.3	19
16	Genetic characterization of novel and CRISPR-Cas9 gene edited maize brachytic 2 alleles. <i>Plant Gene</i> , 2020, 21, 100198.	2.3	8
17	The nucleus-encoded factor MCD4 participates in degradation of nonfunctional 3' UTR sequences generated by cleavage of pre-mRNA in <i>Chlamydomonas</i> chloroplasts. <i>Molecular Genetics and Genomics</i> , 2007, 277, 329-340.	2.1	7
18	Analysis of the <i>Agrobacterium tumefaciens</i> pTiChry5 6b Promoter. <i>Journal of Plant Biochemistry and Biotechnology</i> , 2003, 12, 87-91.	1.7	1