

Circular RNAs more common than previously thought

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In the classical model of gene expression, the genetic script encoded in our genomes is expressed in each cell in the form of RNA molecules, each consisting of a linear string of chemical "bases". It may be time to revise this traditional understanding of human gene expression, as new research suggests that circular RNA molecules, rather than the classical linear molecules, are a widespread feature of the gene expression program in every human cell. The results are published in the Feb. 1 issue of the online journal *PLoS ONE*.

A group of researchers working with HHMI investigator and biochemistry professor Patrick Brown, of Stanford University, have discovered hundreds of human gene transcripts that appear to have resulted from a non-canonical program that "splices" the [RNA molecules](#) into circles. For many genes, these circular RNAs made up a substantial fraction of all the transcripts identified, suggesting that they are far more abundant and perhaps more important than previously thought.

Circular RNAs have heretofore "flown under the radar" because traditional methods for isolating RNA from cells have inadvertently discarded these circular molecules. The exact function of circular RNAs, and potential relevance for human biology or health, if any, remains to be determined, but this study opens up many exciting avenues for further research.

"This research shows that there are still important fundamental biological programs to be discovered by experimental exploration

coupled with new statistical and [computational approaches](#)," said Julia Salzman, one of the authors of the paper. "These circular RNAs may represent a yet-to-be discovered biological process."

More information: Salzman J, Gawad C, Wang PL, Lacayo N, Brown PO (2012) Circular RNAs Are the Predominant Transcript Isoform from Hundreds of Human Genes in Diverse Cell Types. PLoS ONE 7(2): e30733. [doi:10.1371/journal.pone.0030733](https://doi.org/10.1371/journal.pone.0030733)

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