

ERRORS IN BIOLOGY EXTENDS WELL BEYOND DNA MUTATIONS.

We usually think about errors in terms of mutations in DNA. But DNA replication and transcription are actually the most accurate steps in gene expression.

One overlooked error is the "nonsense error": a ribosome falls off the mRNA before finishing the protein, wasting the energy spent on a useless, incomplete chain. A study in PLOS Genetics (1) modeled this per codon in yeast and found the drop-off rate varies enormously, especially for codons resembling stop codons. Yeast genomes seem adapted to manage this cost, avoiding risky codons near the 5'-end of coding sequences and in highly expressed genes.

A related story: slow codon decoding doesn't just risk dropped ribosomes, it can also mark the mRNA itself for destruction. A Spotlight in Trends in Genetics (2) describes how a newly found factor, DHX29, senses sluggish decoding at nonoptimal codons and flags the mRNA for decay, working alongside a second reader, CNOT3, that watches for slow arginine codons elsewhere on the ribosome.

Same root cause, two outcomes: slow decoding can cost a protein or cost the whole transcript. Errors and inefficiencies in **reading** the code turn out to matter as much as mutations in it.

1. <https://journals.plos.org/plosgenetics/article?id=10.1371/journal.pgen.1012162>
2. [https://www.cell.com/trends/genetics/fulltext/S0168-9525\(26\)00149-6?_returnURL=https%3A%2F%2Flinkinghub.elsevier.com%2Fretrieve%2Fpii%2FS0168952526001496%3Fshowall%3Dtrue](https://www.cell.com/trends/genetics/fulltext/S0168-9525(26)00149-6?_returnURL=https%3A%2F%2Flinkinghub.elsevier.com%2Fretrieve%2Fpii%2FS0168952526001496%3Fshowall%3Dtrue)